

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 12:40:35 ; Search time 13047 Seconds
(without alignments)
1225.650 Million cell updates/sec

Title: US-10-667-289-1
Perfect score: 2857.4
Sequence: 1 gctgtagcggagattccatcgt.....gctcgtgaaaaaaaaaaaaa 2859

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST.*
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589.6	20.6	651	14	AG176412 Pan trogl
2	562.4	19.7	757	7	BP211696 601812317
3	522.2	18.3	842	3	BP183992 601843003
4	501.8	17.6	583	3	BP282008 BP282008
5	499.6	17.5	602	5	CD708943 EST25470
6	488.4	17.1	628	14	AG154727 Pan trogl
7	482.6	16.9	754	7	BP210400 601874484
8	474.2	16.6	917	7	BP238439 601904735
9	448.8	15.7	820	7	BP209716 601874259
10	428	15.0	823	7	BP238869 601904492
11	424.8	14.9	825	12	CC496590 CH240_332
12	353	12.4	916	3	BQ228535 AGENCOURT
13	345.6	12.1	513	7	BP239183 601905584
14	316.2	11.1	720	4	CB429984 605838 MA
15	268.2	9.4	540	7	BP212748 601813991
16	252.4	8.8	559	11	AG689233 HS_5565_A
17	247.8	8.7	438	11	AG678212 HS_5518_B
18	246.2	8.6	537	9	DB302402 DB302402
19			870	11	AQ739907 HS_5506_A

C 20	245.8	8.6	635	14	DU666845 Clufl-HI
C 21	243.8	8.5	557	11	AQ674674 HS_5485_B
C 22	243.6	8.5	946	11	AQ744276 HS_5508_A
C 23	243.2	8.5	539	7	AM500534 UI-HP-BN0
C 24	243.2	8.5	604	3	BM990713 UI-H-D10-
C 25	242.8	8.5	403	2	BM941633 ax15d09.x
C 26	242.6	8.5	446	7	BE140949 MRO-HT006
C 27	242.6	8.5	1270	6	BC016019 Homo sapi
C 28	242	8.5	472	9	DA156998 DA156998
C 29	241.8	8.5	471	1	AI753904 AI753904
C 30	241.8	8.5	522	3	BU727226 UI-E-CR0-
C 31	241.8	8.5	562	3	BQ638837 hd28b12.y
C 32	241.8	8.5	704	14	AG113471 Pan trogl
C 33	241.8	8.5	1336	6	BG674233 602619894
C 34	241.6	8.5	2535	6	AF464877 Homo sapi
C 35	241.6	8.5	530	9	DA804882 DA804882
C 36	241.6	8.5	530	9	DA804558 DA804558
C 37	241.6	8.5	575	9	DB078664 DB078664
C 38	241.6	8.5	579	14	DU666109 Clufl-HI
C 39	241.6	8.5	1159	2	BM465227 AGENCOURT
C 40	241.4	8.4	757	3	BQ429569 AGENCOURT
C 41	241.2	8.4	5037	6	BSM807357 Homo sapi
C 42	240.8	8.4	376	3	BM672810 UI-E-C00-
C 43	240.8	8.4	583	3	BP330444 BP330444
C 44	240.6	8.4	519	4	BX503510 BX503510
C 45	240.6	8.4	662	14	DU840715 MUQO_CH25

ALIGNMENTS

RESULT 1
AG176412
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-047K09.T7, genomic survey
ACCESSION AG176412
VERSION AG176412.1 GI:16706092
KEYWORDS
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.
TITLE BAC end sequences of Library RP43-43
JOURNAL Unpublished
2 (bases 1 to 651)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RP43-43 This BAC end was generated during the Red process and may have higher chance of clone tracking errors.

PRIMERS
LIBRARY
Sequencing: T7
Vector : pBACE3.6
R.site 1 : EcoRI
R.site 2 : EcoRI
Location/Qualifiers
1. 651
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-047K09.T7"

FEATURES

source

ORIGIN /sex="male"
/cell_type="lymphocytes"
/clone_lib="RPI-43 Chimpanzee Male BAC Library"

Query Match 20.6%; Score 589.6; DB 14; Length 651;
Best Local Similarity 97.9%; Pred. No. 4.1e-79;
Matches 617; Conservative 1; Mismatches 10; Indels 2; Gaps 2;

QY 1747 AATATTTCTGGGAATTAAGCTCATTAATTAATCAAGGAATGCAAGTCTCTGACAT 1806
DB 24 AATATTTCTGGGAATTAAGCTCATTAATTAATCAAGGAATGCAAGTCTCTGACAT 83
QY 1807 ACAAACTCAGTAGAGAGAGAAACCAACATGCTTTTGGAAAATGATTCACCCAGTGAAC 1866
DB 84 ACAAACTCAGTAGAGAGAGAAACCAACATGCTTTTGGAAAATGATTCACCCAGTGAAC 143
QY 1867 TATTCAGAAACAGACCTGCTTCTGTAATGATTTGCTCTGTTGGGAATGTAATGA 1926
DB 144 TATTCAGAAACAGACCTGCTTCTGTAATGATTTGCTCTGTTGGGAATGTAATGA 203
QY 1927 GAGGTGGCATTAATTAATTAATTTTCCAAAATATTTGGAAAGCACTTCAATAG 1986
DB 204 GAGGTGGCATTAATTAATTAATTTTCCAAAATATTTGGAAAGCACTTCAATAG 263
QY 1987 GATTTCACTTGGAAAAGTAGAGCTGTGTCAAAATCAATATGAGAAAGCTGCTTG 2046
DB 264 GATTTCACTTGGAAAAGTAGAGCTGTGTCAAAATCAATATGAGAAAGCTGCTTG 323
QY 2047 CAATCTGAACCTGGGTTTCCCTGCAATAGAAATGAAATTCCTCTTTTGAAGAAA 2106
DB 324 CAATCTGAACCTGGGTTTCCCTGCAATAGAAATGAAATTCCTCTTTTGAAGAAA 383
QY 2107 TGAATTCACATTAATAATCTTCAATGACACATGTTTCAATTCCTGATTAATACCT 2166
DB 384 TGAATTCACATTAATAATCTTCAATGACACATGTTTCAATTCCTGATTAATACCT 443
QY 2167 AGGTAGGGAGTTGCTGGGCAATAGATATGATTTGATTTGATTTGATTTGATTTG 2226
DB 444 AGGTAGGGAGTTGCTGGGCAATAGATATGATTTGATTTGATTTGATTTGATTTG 503
QY 2227 CAGAGTAGTACATTTCTGTGCTCTACATCAACATGAAATTCCTGGAGCTTCAT 2286
DB 504 CAGAGTAGTACATTTCTGTGCTCTACATCAACATGAAATTCCTGGAGCTTCAT 563
QY 2287 GCCTTTTATTTTAAAGCATTTCTGCTGCTTCTTAAATTAAGAAATTAAGTCCC 2346
DB 564 GCCTTTTATTTTAAAGCATTTCTGCTGCTTCTTAAATTAAGAAATTAAGTCCC 622
QY 2347 GAAAGTGAACATGCTTCATGTCACACAT 2376
DB 623 GAAAGTGAACATGCTTCATGTCACACAT 651

RESULT 2
BF211696 757 bp mRNA linear EST 06-NOV-2000
LOCUS 601812317F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4046500 5',
DEFINITION mRNA sequence.
ACCESSION BF211696
VERSION BF211696.1 GI:11105282
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 757)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov

FEATURES
source
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
Plate: LINC874 row: b column: 05
High quality sequence stop: 648.
Location/Qualifiers
1..757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4046500"
/issue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_54"
/note="Organ: Bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcggcggcggc); Site 2: SfiI
(ggccatcgcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTAGGCC-3' and
3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Query Match 19.7%; Score 562.4; DB 7; Length 757;
Best Local Similarity 97.7%; Pred. No. 5e-75;
Matches 643; Conservative 1; Mismatches 7; Indels 7; Gaps 7;

QY 1686 GGTATCAAAAGCATCTTAATTTGCTTTTGTTCAGATGTAATTCATGAACA 1745
DB 1 GGTATCAAAAGCATCTTAATTTGCTTTTGTTCAGATGTAATTCATGAACA 59
QY 1746 CAATATTTCTGGAGAAATTAAGCTCATTAATTAATCAAGAAATTCCTGACCA 1805
DB 60 CAATATTTCTGGAGAAATTAAGCTCATTAATTAATCAAGAAATTCCTGACCA 119
QY 1806 TACAAAACCTCAGTAGAGAGAGAAACCAACATGCTTTTGAAGAAATGATCACCCAGTGA 1865
DB 120 TACAAAACCTCAGTAGAGAGAGAGAAACCAACATGCTTTTGAAGAAATGATCACCCAGTGA 178
QY 1866 CTATTCAGAAACAGACCTGCTTCTGTAATTTGCTCTGTTGGGATCTGAATG 1925
DB 179 CTATTCAGAAACAGACCTGCTTCTGTAATTTGCTCTGTTGGGATCTGAATG 236
QY 1926 AGGAGTTGCACTTATTAATTAATTTTCCAAATAATTTGGAAAGCACTTCAATA 1985
DB 237 AGGAGTTGCACTTATTAATTAATTTTCCAAATAATTTGGAAAGCACTTCAATA 295
QY 1986 GGAATTCACCTTGGAAAAGTAGAGCTGTGTCAAAATCAATATGAGAAAGCTGCTT 2045
DB 296 GGAATTCACCTTGGAAAAGTAGAGCTGTGTCAAAATCAATATGAGAAAGCTGCTT 355
QY 2046 GCAATCTGAACCTGGGTTTCCCTGCAATAGAAATGAAATTCGCTCTTTTGAAGAAA 2105
DB 356 GCAATCTGAACCTGGGTTTCCCTGCAATAGAAATGAAATTCGCTCTTTTGAAGAAA 415
QY 2106 ATGTATTCACATCAAAATCTTCAATGACACATGTTTCAATTCCTGATTAATAC 2165
DB 416 ATGTATTCACATCAAAATCTTCAATGACACATGTTTCAATTCCTGATTAATAC 475
QY 2166 TAGGTAGGGATGCTGGGCAATATGATATGATATGTTTCAATCTTACCAATCT-TGT 2224
DB 476 TAGGTAGGGATGCTGGGCAATATGATATGATATGTTTCAATCTTACCAATCTGTGT 535
QY 2225 TCCAGAGTAGTACATTTCTGTGCTCTACATCACCATGTAGAAATTCCTGGAGCTCC 2284

Db 536 TCACAGATAGTGCATTTCTGTGCTCTACCATCATCATGTAAGAAATCCCGGAGCTCC 595

Qy 2285 ATGCTTTAAATTTTGGCATCTTCT-T-GCTMAATTTCTTAAATAGAAATTAG 2341

Db 596 ATGGCTTTAAATTTTGGCATCTCTGCTGCTCATTTCTTAAATTAAGATTACAG 653

RESULT 3
BF183992

LOCUS BF183992 842 bp mRNA linear EST 31-OCT-2000

DEFINITION 601843003F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4063848 5', mRNA sequence.

ACCESSION BF183992

VERSION BF183992.1 GI:11062336

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 842)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgsabers-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: <http://image.llnl.gov>

Plate: LHC697 row: e column: 01

High quality sequence stop: 635.

Location/Qualifiers

1. 842

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4063848"

/issue_type="from chronic myelogenous leukemia"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_54"

/note="Origin: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcggctcgcc); Site 2: SfiI (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 18.3%; Score 522.2; DB 7; Length 842;

Best Local Similarity 96.3%; Pred. No. 5.5e-69;

Matches 673; Conservative 0; Mismatches 13; Indels 13; Gaps 13;

Qy 1553 GATCTCAACCTGATATTAACCCCAATTTTCCTGCTGAGGAGGACCATCTC 1612

Db 1 GATCTCAACCTGATATTAACCCCAATTTTCCTGCTGAGGAGGACCATCTC 60

Qy 1613 AGCATATATATGAATTTACTCTCTTAACCTTAAACACAGTTGATCTTGAAGTCA 1672

Db 61 AGCATATATATGAATTTACTCTCTTAACCTTAAACACAGTTGATCTTGAAGTCA 120

Qy 1673 GGAATATATCCAGGTTACAAAGCATCTTAATTTTCCTTTTCTGTTTCAAGTGAAT 1732

Db 121 GGAATATATCCAGGTTACAAAGCATCTTA-TTGTCTTTTCTGTTCAGTGAAT 179

Qy 1733 TCATAGAGCAACACATATTTCTTGGAGATTAAGCTCATATTAATCAAGAGATGC 1792

Db 180 TCATAGAGCAACACATATTTCT-TGAGATTTAAGCTCATATTAATCAAGAGATGC 238

Qy 1793 AGTTCTCTGACATACAAAATCAGTAGAGAGAAACCAATGCTTTTGGAAATGAT 1852

Db 239 AGTTCTCTGACATACAAAATCAGTAGAGAGAAACCAATGCTTTTGGAAATGAT 297

Qy 1853 TCACCCAGTAAACCTATTTCCAGAACAGACCTCTCTGATTAATTTGCTCTGTTG 1912

Db 298 TCACCCAGTAAACCTATTTCCAGAACAGACCTCTCTGATTAATTTGCTCTGTTG 355

Qy 1913 GGGATGATGATAGAGAGTTGGCCATTAATTAATTAATTTTCCAAAATTA-TTGGAA 1972

Db 356 GGGATGATGATAGAGAGTTGGCCATTAATTAATTAATTTTCCAAAATTA-TTGGAA 414

Qy 1973 AGCCACTTCAATAGATTTTCACTCTTGGAAAGTAGAGCTGTGTGCAAAATCAATATG 2032

Db 415 AGCCACTTCAATAGATTTTCACTCTTGGAAAGTAGAGCTGTGTGCAAAATCAATATG 474

Qy 2033 AGAAAGCTGCTTGCATCTGAACCTTGGCTTCCGCAATAGAAATTTGATTTGCTT 2092

Db 475 AGAAAGCTGCC-TGCATCTGAAC-TGGGTTTCCCTGCAATAGAAATTTGATTTG-CT 531

Qy 2093 CTTTGGAAAAAATGATTTCACTCAATCAATCTTCCATGAGACATGTTTCAATTTCC 2152

Db 532 CTTTGGAAAAAATGATTTCACTCAATCAATCTTCCATGAGACATGTTTCAATTTCC 591

Qy 2153 TTGATTAATATACCTAGATAGGAGGATTTGGGCGCATATGATTAAGATTTCAAGTTCT 2212

Db 592 TTGATTAATTA-CTAAGTAGGAGATTTGGTGG-CATATGATTAAGCATATG-TCCAGTTCT 648

Qy 2213 ACCAATCTTGTTCAGAGATGATGACATTTCTGTCTCC 2251

Db 649 ACC-ATCTTGTTCAGAGATGATGACATTTCTGTCTCAC 686

RESULT 4
BP282008

LOCUS BP282008 583 bp mRNA linear EST 16-SEP-2004

DEFINITION clone KMR03033, mRNA sequence.

ACCESSION BP282008

VERSION BP282008.1 GI:52195740

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 583)

Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL PUBMED 15342556

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Tel: 81-3-5449-5343

Fax: 81-3-5449-5416

Email: ysuzuki@hgc.jp.

Location/Qualifiers

1. 583

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KMR03033"

/issue_type="bone marrow"

ORIGIN
/cell_line="K562"
/clone_lib="Sugano cDNA library, bone marrow K562"
/note="chronic myelogenous leukemia"

Query Match 17.6%; Score 501.8; DB 3; Length 583;

Best Local Similarity 98.6%; Pred. No. 7.3e-66; Mismatches 7; Indels 0; Gaps 0;

Matches 506; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 903 ACCAACTGGAGTGTAAAGATTGACACCAATTTTACATATGTCAGCAAGTCAGAT 962
DB 71 AGCAGTGTGAACTGTGTAAGATTGACACCAATTTTACATATGTCAGCAAGTCAGAT 130
QY 963 TCTACTGGAGCCAAACATTAGTATGTTCAAGTATGTCAGCAAGTCAGCAAGT 1022
DB 131 TCTACTGGAGCCAAACATTAGTATGTTCAAGTATGTCAGCAAGTCAGCAAGT 190
QY 1023 GGTACTGGAGCCCTTGGAGTTCAACCTTTTTCATTAACCTGAAACAGTTCCCAAG 1082
DB 191 GGTACTGGAGCCCTTGGAGTTCAACCTTTTTCATTAACCTGAAACAGTTCCCAAG 250
QY 1083 TCACATCAAAAGAGATTCACATGACATGAAATTCGGCTTACAGTTGCTTCATCT 1142
DB 251 TCACATCAAAAGAGATTCACATGACATGAAATTCGGCTTACAGTTGCTTCATCT 310
QY 1143 CTACAGGGCACTTACTTCTGACACAGAGAGACATTTGATTTTATGGAGATGATCG 1202
DB 311 CTACAGGGCACTTACTTCTGACACAGAGAGACATTTGATTTTATGGAGATGATCG 370
QY 1203 TCTTTGCTGTATGTTGTCATCTTCTTCTTGTATGGAGATTTTAAACATCTCCGAA 1262
DB 371 TCTTTGCTGTATGTTGTCATCTTCTTCTTGTATGGAGATTTTAAACATCTCCGAA 430
QY 1263 CTGGAGTTAAAGAGATCTTATGTTTATACCAAGTGGCTTTATGAAGATTTCTTA 1322
DB 431 CTGGAGTTAAAGAGATCTTATGTTTATACCAAGTGGCTTTATGAAGATTTCTTA 490
QY 1323 ATATGAAAAACAGCAATGTTGTAAAAATGCTACAGAAAAATAGTGAATTAATA 1382
DB 491 ATATGAAAAACAGCAATGTTGTAAAAATGCTACAGAAAAATAGTGAATTAATA 550
QY 1383 ATTCCAGTGAAGAGTCTTATGTTGATCCCA 1415
DB 551 ATTCCAGTGAAGAGTCTTATGTTGATCCCA 583

RESULT 5
CD708943 602 bp mRNA linear EST 25-JUN-2003

LOCUS EST25470 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD708943
CD708943.1 GI:32239573

DEFINITION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 602)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center

Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510600, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

FEATURES
1. .602
location/Qualifiers
/organism="Homo sapiens"

ORIGIN
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="RSTS generated from a normal nasopharynx cDNA
library from southern Chinese"

Query Match 17.5%; Score 499.6; DB 5; Length 602;

Best Local Similarity 99.8%; Pred. No. 1.6e-65; Mismatches 0; Indels 0; Gaps 0;

Matches 499; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 28 CAGCCAAACAAGGTTGACAGCTGCTCTGTAAGTGAATTTATGCTTCAACAGGTTGAA 87
DB 103 CAGCCAAACAAGGTTGACAGCTGCTCTGTAAGTGAATTTATGCTTCAACAGGTTGAA 162
QY 88 AGAGGGAACAGCTTTCTGCTTCCAGACATGAAATGACATGCTTCAATGGAGATGC 147
DB 163 AGAGGGAACAGCTTTCTGCTTCCAGACATGAAATGACATGCTTCAATGGAGATGC 222
QY 148 AGTAATAGCCCTTTTACATCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 207
DB 223 AGTAATAGCCCTTTTACATCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 282
QY 208 CTCTGGCCCACTCTGGGTGAAACAGCCCAATTTTAAAGTGGATGATATCTCTAT 267
DB 283 CTCTGGCCCACTCTGGGTGAAACAGCCCAATTTTAAAGTGGATGATATCTCTAT 342
QY 268 ATATTGCGAAGAGCAATTTAAGATGAGCTGCAACCAAGAACTTCATTTTATATAAATGG 327
DB 343 ATATTGCGAAGAGCAATTTAAGATGAGCTGCAACCAAGAACTTCATTTTATATAAATGG 402
QY 328 CATCAAGAAAGATTTCAATCAACCAAGATTAATAAACAAGCTGCGCTTTGGATATA 387
DB 403 CATCAAGAAAGATTTCAATCAACCAAGATTAATAAACAAGCTGCGCTTTGGATATA 462
QY 388 AAATCTTCTGGAACCAAGCTCTTCTATGTCAGTCTGTCAGTCTGTCAGTCTGTCAG 447
DB 463 AAATCTTCTGGAACCAAGCTCTTCTATGTCAGTCTGTCAGTCTGTCAGTCTGTCAG 522
QY 448 AGAGACATGATATGAGAAAGACATTTCTTCTGATATCCGCGAGATATTCCTGATGA 507
DB 523 AGAGACATGATATGAGAAAGACATTTCTTCTGATATCCGCGAGATATTCCTGATGA 582
QY 508 AGTAACCTGTCATTTATG 527
DB 583 AGTAACCTGTCATTTATG 602

RESULT 6
AG154727 628 bp DNA linear GSS 09-JAN-2002

LOCUS AG154727
DEFINITION Pan troglodytes DNA, clone: RP43-018N08.T7, genomic survey
sequence.
AG154727
AG154727.1 GI:16684405

ACCESSION GSS.
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes

ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE BAC end sequences of library RRC1-43
JOURNAL Unpublished
2 (bases 1 to 628)

REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

COMMENT

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimbes@sec.riken.go.jp, URL: http://hgp.sec.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI

FEATURES

source

1. 628
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-018N08.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 17.5%; Score 499.6; DB 14; Length 628;
Best Local Similarity 94.3%; Pred. No. 1.5e-65;
Matches 561; Conservative 1; Mismatches 26; Indels 7; Gaps 4;

QY 1743 ACACAAATTTCTTGGAGAAATTAAGCTCAATTAATCAAGAGAAATGAGTTCTCTG 1802
DB 23 ACACAAATTTCTTGGAGAAATTAAGCTCAATTAATCAAGAGAAATGAGTTCTCTG 82
QY 1803 ACATACAAATCTAGTAGAGAGAGAAACCAACGATGTTGGAAATGATTCACCAAGT 1862
DB 83 ACATACAAATCTAGTAGAGAGAGAAACCAACGATGTTGGAAATGATTCACCAAGT 142
QY 1863 AAATCTATTCAGAAACAGACCCCTGCTGATGAATTTGCTCTGTTGGAGATCGTGA 1922
DB 143 AAATCTATTCAGAAACAGACCCCTGCTGATGAATTTGCTCTGTTGGAGATCGTGA 202
QY 1923 ATGAGAGTTGCCATCTTAATTAATCTTAATTTTCCACAAATATTTTGGAAAGCATTCA 1982
DB 203 ATGAGAGTTGCCATCTTAATTAATCTTAATTTTCCACAAATATTTTGGAAAGCATTCA 262
QY 1983 ATGAGATTCACCTTGGAAAGTAGAGCTGTGTGTCATTAATCAATATGAGAAAGCTGC 2042
DB 263 ATGAGATTCACCTTGGAAAGTAGAGCTGTGTGTCATTAATCAATATGAGAAAGCTGC 322
QY 2043 CTTCGCAATCTGAATCTGGTTTCCCTGCAATAGAAATTAATTTGCTCTTTTGGAA 2102
DB 323 CTTCGCAATCTGAATCTGGTTTCCCTGCAATAGAAATTAATTTGCTCTTTTGGAA 382
QY 2103 AAAATGATTCACATCAAAATCTTCACATGAGACACATGTTTCAATTTCCCTGGATTAAT 2162
DB 383 AAAATGATTCACATCAAAATCTTCACATGAGACACATGTTTCAATTTCCCTGGATTAAT 442
QY 2163 ACTAGTAGAGGATGCTGGGCAATAGATAGATATTTCAAGTTCAACAA--TCT 2220
DB 443 ACTAGTAGAGGATGCTGGGCAATAGATAGATATTTCAAGTTCAACAA--TCT 502
QY 2221 TGTTCAGAGTAGTACACA--TTTCTGTGCTCTACACATCAACATGTAA--GAAATCCCGGG 2278
DB 503 GGTTCAGAGTAGTACACA--TTTCTGTGCTCTACACATCAACATGTAA--GAAATCCCGGG 562
QY 2279 AGCTCCATGCTTTTAA--TTTATGCAATCTTCTGCTCAATTTCTTAAAT 2330
DB 563 AGCTCCATGCTTTTAA--TTTATGCAATCTTCTGCTCAATTTCTTAAAT 617

RESULT 7

BF210400

LOCUS BF210400 754 bp mRNA linear EST 06-NOV-2000
DEFINITION 601874484F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101164 5',
mRNA sequence.

ACCESSION

BF210400 GI:11103986

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 754)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNC972 row: 9 column: 21
High quality sequence stop: 650.
Location/Qualifiers
1. 754
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4101164"
/issue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 54"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccggccg); Site 2: SfiI
(ggccatcggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGCCATTATGAGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

FEATURES

source

1. 754
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4101164"
/issue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 54"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccggccg); Site 2: SfiI
(ggccatcggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGCCATTATGAGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Query Match 17.1%; Score 488.4; DB 7; Length 754;
Best Local Similarity 93.7%; Pred. No. 7.1e-64;
Matches 564; Conservative 0; Mismatches 31; Indels 7; Gaps 5;

QY 903 ACCAACTTGAATGTTAAAGAAATTTGACACCAATTTTCAATATGTCGAACATCGAAT 962
DB 71 AGCCAGTGTGAACTGTTAAAGAAATTTGACACCAATTTTCAATATGTCGAACATCGAAT 130
QY 963 TCTACTTGGAGCAACATTAAGTAGTATTTCAAGTAGATGTCAAGAAACAGCAAAA 1022
DB 131 TCTACTTGGAGCAACATTAAGTAGTATTTCAAGTAGATGTCAAGAAACAGCAAAA 190
QY 1023 GGTACTGGAGGCTTGGAGTCAACGTTTTCATTAACCACTGAAACATTTCCCAAG 1082
DB 191 GGTACTGGAGGCTTGGAGTCAACGTTTTCATTAACCACTGAAACATTTCCCAAG 250
QY 1083 TCACATCAAAAGATTCACAAACATGACACATGAAATCTGGGCTTAACAGTTGCTTCATCT 1142
DB 251 TCACATCAAAAGATTCACAAACATGACACATGAAATCTGGGCTTAACAGTTGCTTCATCT 310
QY 1143 CTACAGGAGCACTTACTTGAACAACAGAGAGACATTTGATTTTATTTGGAAATGTC 1202
DB 311 CTACAGGAGCACTTACTTGAACAACAGAGAGACATTTGATTTTATTTGGAAATGTC 370
QY 1203 TCTTGTCTGTATGTGTCAATTTCTTTGATTTGGATTTTAAACATCATCTCCGAA 1262
DB 371 TCTTGTCTGTATGTGTCAATTTCTTTGATTTGGATTTTAAACATCATCTCCGAA 430

QY 1263 CTGGATTAAAGAGATCTTATTTGTTATACCAAGTGGCTTTATGAGATATTCCTA 1322
 DB 431 -TGGATTAAAGAGATCTTATTTGTTATACCAAGTGG-TTTATGAGATATTCCTA 488
 QY 1323 AATGAAAAACAGCAATGTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 1382
 DB 489 AATGAAAAACAGCAATGTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 548
 QY 1383 ATTCAGTGGAGCGTCTATATGTTGATCCATGATTAACAGATTAAGAAATCTCA 1442
 DB 549 ATTCAGTGGAGCGT-CTATATGTTGATCCATGATTAACAGATTAAGAAATCTCA 607
 QY 1443 TCCAGAACACAGCCTACAGCTACAGAGAGAAATACAGAGCCCTGGACAGAG 1502
 DB 608 TCC---AGAACAAAGTACAGACTACAGAGAG-GAATACAGAGCCCTGGACAGAGAT 663
 QY 1503 AC 1504
 DB 664 AC 665

RESULT 8
 LOCUS BF238439 917 bp mRNA linear EST 14-NOV-2000
 DEFINITION 601904735F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132593 5',
 mRNA sequence.

ACCESSION BF238439
 VERSION BF238439.1 GI:11152359
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 917)
 NIH_MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.jnl.gov
 Plate: LNCM1032 row: e column: 10
 High quality sequence stop: 575.
 Location/Qualifiers

FEATURES
 source

1.917
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4132593"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_54"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: Sf11 (ggcgcctcgcc); Site 2: Sf11
 (ggccatctggcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGGCATATATGGCC-3' and
 3' adaptor sequence: 5'-ATCTAGAGCGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

Query Match 16.9%; Score 482.6; DB 7; Length 917;
 Best Local Similarity 90.5%; Pred. No. 5e-63;
 Matches 583; Conservative 0; Mismatches 50; Indels 11; Gaps 6;

QY 903 ACCAACTTGGAAATGTTAAGAAATTTGACACCAATTTTCATATGTGCAACGTGGAAT 962
 DB 71 AGCATGTGAACCTGTTAAAGAAATTTGACACCAATTTTCATATGTGCAACGTGGAAT 130
 QY 963 TCTACTTGGAGCCAAACATTAAGTACGTATTTCAAGTGAATGTCAAGAAACAGGCAAA 1022
 DB 131 TCTACTTGGAGCCAAACATTAAGTACGTATTTCAAGTGAATGTCAAGAAACAGGCAAA 190
 QY 1023 GGTACTGCGACGCTTGGAGTTCAACGTTTTTTCATAAACAGCTGAACAGTTCCCAAG 1082
 DB 191 GGTACTGCGACGCTTGGAGTTCAACGTTTTTTCATAAACAGCTGAACAGTTCCCAAG 250
 QY 1083 TCACATCAAAAGCATTCGCAACATGACATGGAATCT--GGGCTAACAGTGGCTTCATC 1141
 DB 251 TCACATCAAAAGCATTCGCAACATGACATGGAATCTGGGGCTAACAGTGGCTTCATC 310
 QY 1142 TCTACAGGCGACCTTACTTCTGACCAAGAGAGACATTGACCTTTATTTGGGAATGATC 1201
 DB 311 TCTACAGGCGACCTTACTTCTGACCAAGAGAGACATTGACCTTTATTTGGGAATGATC 370
 QY 1202 GTCTTGTCTGTATATGTTGCAATCTTTCTTTGATTTGGGATATTTAAACAGATTCCTGA 1261
 DB 371 GTCTTGTCTGTATATGTTGCAATCTTTCTTTGATTTGGGATATTTAAACAGATTCCTGA 430
 QY 1262 ACTGGATTAAAGAAAGATCTTATTTGTTAATCCAAAGTGGCTTATGAAATATTCCT 1321
 DB 431 ACTGGATTAAAGAAAGATCTTATTTGTTAATCCAAAGTGGCTTATGAAATATTCCT 488
 QY 1322 AATATGAAAAACAGCAATGTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 1381
 DB 489 AATATGAAAAACAGCAATGTTGAAAAATGCTACAGAAAAATAGTGAATTAATAA 548
 QY 1382 AATTCAG-TGAGCAGGTCCTATATGTTGATCCCATGATTAACAGATTAAGAAATCTT 1440
 DB 549 AATCCAGTTGAGCAGGTCCTATATGTTGATCCCATGATTAACAGATTAAGAAATCTT 608
 QY 1441 CATCCGAAACCAAGCCTACAGACTACAGAAAGAGAAATTAACAGAGCCCTGGAGCAAG 1500
 DB 609 TCATCCGAAACCAAGCCTACAGACTACAGAAAGAGAAATTAACAGAGCCCTGGAGCAAG 665
 QY 1501 AGACTACCCGCAAAACTCGCTATTCGACAATCTACAGTGTAT 1544
 DB 666 AGATAAC-----GAATCGCTATTCGAAAAATCTACAGGTAT 705

RESULT 9
 LOCUS BF209716 820 bp mRNA linear EST 06-NOV-2000
 DEFINITION 601874259F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4098831 5',
 mRNA sequence.

ACCESSION BF209716
 VERSION BF209716.1 GI:11103302
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 820)
 NIH_MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

ORIGIN

QY 1022 AGGTACTGGAGCGCTTGAAGTTCACCGTTTTCATATAAACAACCTGAACAGTTCGCCAG 1081
 DB 188 AGGTACTGGAGCGCTTGAAGTTCACCGTTTTCATATAAACAACCTGAACAGTTCGCCAG 247
 QY 1082 GTTCACATCAAAAGCATTCACATGACACATGGAATTTCTGGCTTACAGTTCCTTCATC 1141
 DB 248 GTTCACATCAAAAGCATTCACATGACACATGGAATTTCTGGCTTACAGTTCCTTCATC 307
 QY 1142 TCTACAGGGGACCTTCTCTGACCAACAGAGAGACATTCGACTTTTA-TTGGGAATGAT 1200
 DB 308 TCTACAGGGGACCTTCTCTGACCAACAGAGAGACATTCGACTTTTA-TTGGGAATGAT 367
 QY 1201 CGTCTTGTGCTTATGTTGCAATTCCTTCTTGTGATGGATTTTAAACAGATCATTCGC 1260
 DB 368 CGTCTTGTGCTTATGTTGCAATTCCTTCTTGTGATGGATTTTAAACAGATCATTCGC 427
 QY 1261 AACTGGATTTAAAGAAAGCATTTATTTGTAATACCAAGTGGCTTTATGAATATTC 1320
 DB 428 AACTGGATTTAAAGAAAGCATTTATTTGTAATACCAAGTGGCTTTATGAATATTC 486
 QY 1321 TAATATGAATAAAGCAATGTTGTAATAATGCTACAGAAATAA-TGGAATATGTAAT 1379
 DB 487 TAATATGAATAAAGCAATGTTGTAATAATGCTACAGAAATAA-TGGAATATGTAAT 545
 QY 1380 ATTAATTCAGTGAAGAGTCTTATATGTTGATCCATGATTTACAGATTAAGAAATCT 1439
 DB 546 ATTAATTCAGTGAAGAGTCTTATATGTTGATCCATGATTTACAGAT-TAAGAAATCT 603
 QY 1440 TCATCCCAAGACCAAGCTTACGA 1464
 DB 604 TCAT-CCAGAACCAAGCTTACGA 627

RESULT 11
 CC496590 825 bp DNA linear GSS 17-JUN-2003
 LOCUS CH240_332J15.TARBA13P2 CHORI-240 Bos taurus genomic clone
 DEFINITION CH240_332J15, genomic survey sequence.
 ACCESSION CC496590
 VERSION CC496590.1 GI:31811154
 KEYWORDS GSS.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 825)
 Holt,R., Stolt,J., Yang,G., Barber,S., Smalhus,D., Prabhu,A.-L.,
 Tsai,M., Cloutier,A., Lee,D., Gilm,N., Olson,T., Mayo,M.,
 Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A.,
 Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
 Schein,J., Marra,M., de Jong,P., McMillan,S., Barris,W.,
 Dalrymple,B.P. and Tellam,R.
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 Unpublished (2003)
 Other GSSs: CH240_332J15.T7
 Contact: Rob Holt
 COMMENT
 Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccsc.ca
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Science Centre, Canada.
 Plate: 332 row: J column: 15

Seq primer: SPE
 Class: BAC ends.
 Location/Qualifiers
 1..825
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 /mol_type="genomic DNA"
 /strain="bred: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_332J15"
 /sex="Male"
 /cell_type="Blood"
 /clone_11b="CHORI-240"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull H1 Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

Query Match 15.0%; Score 428; DB 12; Length 825;
 Best Local Similarity 78.3%; Pred. No. 8,9e-55;
 Matches 545; Conservative 0; Mismatches 135; Indels 16; Gaps 2;
 QY 1430 AAAGAATCTTCATCCCAACACAGCTTACAGTACAGAGAG--AGAAATACAGGA 1486
 DB 12 ATGGAATCATTTCTCCAGAGAGAAACCAATGGGCTTACAGAGAGAGAAACAATACAGGA 71
 QY 1487 CCCCTGAGACAAAGAGACTACCCGCAAACTGGCTATTGCAATATCTACAGTTGTAAT 1546
 DB 72 TGCCTGAGAGAGAAAGAGAGAGCTGGAGAAATCACTACACGACCTTACAGTTGTAAT 131
 QY 1547 ATTCTCGATCTCAACCTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGGAAG 1606
 DB 132 ATTCCTGATCTCAACCTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGGAAG 191
 QY 1607 CATCTCAGCAATATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1666
 DB 192 CATCTCAGCAATATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 251
 QY 1667 GACTCAGAAATATATCCAGGTTACAAAGCATCTTAATTTTGTGTTTCTGTTCAAGT 1726
 DB 252 AACTTGGAGAAACATGCCAGGTTAAATAATATCCGATTTTGTGTTTCTGTTCAAGT 311
 QY 1727 GTGAATTCATAGCAACACATATTTCTTGGAGATTAAGCTCATTTAAATCAAGGA 1786
 DB 312 ACAATTCATAGCAACACATATTTCTTGGAGATTAAGCTCATTTAAATCAAGGA 371
 QY 1787 GAATGAGTTCTCTGACATACAAATCTGATGAGAGAGAAACCAATGCTTTTGGAA 1846
 DB 372 GAATGAGTTCTCTGACATACAAATCTGATGAGAGAGAGAAACCAATGCTTTTGGAA 431
 QY 1847 AATGATTCACCAAGGAAATATTCAGAAACAGACCTGCTTCTGATGAAATTTGCTCC 1906
 DB 432 GATGATTCACCAAGGAAATATTCAGAAACAGACCTGCTTCTGATGAAATTTGCTCC 491
 QY 1907 TGTTTGGGAGATGATGAGAGAGGTTGCAATATTAATTAATTTTCCACAAATAT 1966
 DB 492 TGTTTGGGAGATGATGAGAGAGGTTGCAATATTAATTAATTTTCCACAAATAT 551
 QY 1967 TTGGAAGCCACTTCAATAGATTTTCACTTGGAAAAAGTATGATGATGATGATGATGATG 2026
 DB 552 TTGGAAGCCACTTCAATAGATTTTCACTTGGAAAAAGTATGATGATGATGATGATGATG 606
 QY 2027 AATATGAGAAAGCTGCTTGAATGAACTTGGAGTTTCTGCTGCAATGAAATGAAAT 2086
 DB 607 -----AAAGTGCCTTGAATGAAAGAGGCTCTCTCAACCAATTAATTTCT 658
 QY 2087 CTGCTCTTTTGAATAAATAATGATTCATACAA 2122
 DB 659 GCCCAATTTTATTAATTAATGAGATTAAGATCCAA 694
 RESULT 12
 BQ228535 916 bp mRNA linear EST 02-MAY-2002
 LOCUS BQ228535

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DEFINITION  AGENCOURT_7594648 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6061504
5', mRNA sequence.
ACCESSION  B0228535
VERSION    B0228535.1 GI:20409935
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE  1 (bases 1 to 916)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DRP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1AM1331 row: h column: 17
            High quality sequence stop: 554.
            Location/Qualifiers
                1..916
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:6061504"
                /issue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: skin; Vector: PCMV-SPORT6; Site:1: NotI;
                Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
                Technologies."
ORIGIN
Query Match      14.9%; Score 424.8; DB 3; Length 916;
Best Local Similarity 93.1%; Pred. No. 2.6e-54;
Matches 512; Conservative 0; Mismatches 27; Indels 11; Gaps 6;

QY 1258 CCGAAGCTGGATTAAGAGATCTTATGTTATCCAAAGGCTTTATGAAGATAT 1317
    |||
    |||
    |||
DB 221 CTGAAACAGATTAAGAGAGATCTTATGTTATCCAAAGGCTTTATGAAGATAT 280

QY 1318 TCCTAATATGAAGAGAGATGTTGGAAGATGCTACAGAGAAATAGTGAAGCTTATGAA 1377
    |||
    |||
    |||
DB 281 TCTTAATATGAAGAGAGATGTTGGAAGATGCTACAGAGAAATAGTGAAGCTTATGAA 340

QY 1378 TAATAATTCAGTAGAGAGGCTCTATATGTTGATCCCATGATTACAGAGATAAAGAAAT 1437
    |||
    |||
    |||
DB 341 TAATAATTCAGTAGAGAGGCTCTATATGTTGATCCCATGATTACAGAGATAAAGAAAT 400

QY 1438 CTTCATCCCAAGAACAGAGCTTACAGCTACAGAGAGAGATACAGAGACCCCTGAGAC 1497
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    |||
    |||
DB 401 CTTCATCCCAAGAACAGAGCTTACAGCTACAGAGAGAGATACAGAGACCCCTGAGAC 460

QY 1498 AAGAGACTACCGGCAAACTCGCATTCGACATACAGTGTATATATTCCTGATCT 1557
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    |||
    |||
DB 461 AAGAGACTACCGGCAAACTCGCATTCGACATACAGTGTATATATTCCTGATCT 520

QY 1558 CAACACTGATATAACCCCAATTTTCAATTTTCTGCTGAGGAGAGCCATCTCAGCAA 1617
    |||
    |||
    |||
DB 521 CAACACTGATATAACCCCAATTTTCTGCTGAGGAGAGCCATCTCAGCAA 580

QY 1618 TAATAATGAATTAATCTCTTAACACTTAACACCA- GTTGAATCTCTTGAAGCTCAGGAA 1676
    |||
    |||
    |||
DB 581 TAATAATGAATTAATCTCTTAACACTTAACACCA- CGGTTGAATCTCTTGAAGCTCAGGAA 640

QY 1677 ATAATCCA- GGTACAAAGACATCTAATTTGCTTTTCT-- GTTCAAGTGTGAAT 1732

```

```

DB 641 ATAATCCAGGGTTACAAAGACATCTAATTTTCTTTCTGCTCCAAAGGCGAAT 700

QY 1733 T--CACTAAGCAACCAATTTTCT--GGAGATTAAGCCAT--ATTAATCAAGGA 1786
    |||
    |||
    |||
DB 701 TTCCCTAAGCAACCAATTTTCTTTGAGAAATTAAGCTCTCTAATTAATCCAGGGA 760

QY 1787 GAATGAGTT 1796
    |||
    |||
    |||
DB 761 GAATGAGTT 770

RESULT 13
BP239183
LOCUS
DEFINITION  601905584F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133421 5',
            mRNA sequence.
ACCESSION  BP239183
VERSION    BP239183.1 GI:11153104
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE  1 (bases 1 to 513)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1CM1034 row: g column: 22
            High quality sequence stop: 502.
            Location/Qualifiers
                1..513
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4133421"
                /issue_type="from chronic myelogenous leukemia"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_1lb="NIH_MGC_54"
                /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
                Site:1: SfiI (ggcgccctggcc); Site:2: SfiI
                (ggccatctggcc); Double-stranded cDNA was prepared from
                cell line RNA. 5' and 3' adaptors were used in cloning as
                follows: 5' adaptor sequence: 5'-CACGCCATTATGCCC-3' and
                3' adaptor sequence:
                5'-ATTCTAGAGCCGACGCGCCGACAG-G-dT(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size
                1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
                inserts by PCR. This library was enriched for full-length
                clones and was constructed by Clontech Laboratories (Palo
                Alto, CA)."
ORIGIN
Query Match      12.4%; Score 353; DB 7; Length 513;
Best Local Similarity 95.0%; Pred. No. 2.1e-43;
Matches 419; Conservative 0; Mismatches 15; Indels 7; Gaps 5;

QY 903 ACCAACTGGAATGTAAGATTTGACACCAATTTTACATATGTGCAACAGTCAGAAAT 962
    |||
    |||
    |||
DB 73 AGCCATGTGAACTGTTAAGAAATTTGACACCAATTTTACATATGTGCAACAGTCAGAAAT 132

QY 963 TCTACTTGAGCCAAACATTAAGTACGTAATTTCAAGTGAATGCAAGAA--CAGGCAA 1020
    |||
    |||
    |||

```

Db 133 TCTACTTGAGACCAACATTAAAGTACGTATTTCAAGTGAAGTGTCCAGAAACAGGCAAA 192
 QY 1021 AAGGTACTGGACGCTTGG-AGTTACCGTT-TTTTCATTAACACCTGAACAGTTCCTC 1078
 Db 193 AAGGTACTGGACGCTTGGAGTTCAACCGTTGTTTCATTAACACCTGAACAGTTCCTC 252
 QY 1079 CAGGTACATCAAAAGACATTCGAA-CATGACATGGAATTTGGGCTAACAGTTCCTC 1137
 Db 253 CAGGTACATCAAAAGACATTCGAAAGATGACATGGAATTTGGGCTAACAGTTCCTC 312
 QY 1138 CATCTTACAGGGACCTTACTCTTGACACAGAGAGAC-ATTGACCTTTATATGGGA 1195
 Db 313 CATCTTACAGGGACCTTACTCTTGACACAGAGAGACATTTGGAATTTATATGGGA 372
 QY 1196 ATGATGCTCTTCTGTATGTATGTGCAATCTTCTTTGATGGGATTTATTAACAGATCA 1255
 Db 373 ATGATGCTCTTCTGTATGTATGTGCAATCTTCTTTGATGGGATTTATTAACAGATCA 432
 QY 1256 TTCCGAAGCTGGAGTTAAAGAGATCTTAATTTTAATACAAAGTGGCTTTATGAAGAT 1315
 Db 433 TTCCGAAGCTGGAGTTAAAGAGATCTTAATTTTAATACAAAGTGGCTTTATGAAGAT 492
 QY 1316 ATTCTTAATTTGAAAAACAGC 1336
 Db 493 ATTCTTAATTTGAAAAAGAGC 513

RESULT 14
 LOCUS CB429984 720 bp mRNA linear EST 25-MAR-2003
 DEFINITION 605838 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
 ACCESSION CB429984
 VERSION CB429984.1 GI:29205578
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 720)
 Smith,T.P.L., Roberte,A.J., Echenkamp,S.E., Chitko-McKown,C.G.,
 Wray,J.E. and Keele,J.W.
 A second set of bovine ESTs from pooled-tissue normalized libraries
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: FOY8023 row: G column: 9
 Seq primer: TAGAAGGACAGTCGAGG.
 Location/Qualifiers
 1..720
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 6BOV"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including liver, lung, hypothalamus, pituitary, and
 placenta/endometrium."

ORIGIN

Query Match 12.1%; Score 345.6; DB 4; Length 720;
 Best Local Similarity 82.9%; Pred. No. 2.5e-42;
 Matches 393; Conservative 1; Mismatches 80; Indels 0; Gaps 0;

QY 473 ATTTCTTGGAATATCCGACGATATTTCTGATGAAGTAACTGTGTCATTTATGAATAT 532
 Db 626 ATTTTAAAGATGATCCACAGATGTACTTGCACAAAGTGCCTGTAAATTTATGAATAT 567
 QY 533 TGAAGCAATGATGCTTGACCTGGAATGCTGGAACTCACTGATAGACAAATATAC 592
 Db 566 TCTGGCAACATGACTTGTACTGTGAAACATGGAGGCCACTTACATAGACAAAGTAT 597
 QY 593 GTGTGATCATGTGAAAGTTTAAAGACAGAAAGAACCAACAGTATCTCACTGAAGCTAT 652
 Db 506 GTGTGTAGTGAAGATTAAAGACAGAAAGAACCAAGAAATATCTCACTGAAGTATAC 447
 QY 653 ATTAACATCTCCACTGATTTATTAACAAGTGGCAAGAAATGATCTTGTGGTCCAGCA 712
 Db 446 ATTAACATCTCCACTGATTTATTAACAAGTGGCAAGAAATGATCTTGTGGTCCAGCA 387
 QY 713 GCAAGCACTGAGGACATGGAAGATGCAAAACACTGCAATTCACCTGATGATATAGTG 772
 Db 386 TCAAAATGTTCTGGGACATGGAAGATGCAAAACACTGCAATTCACCTGATGATATAGTG 327
 QY 773 ATACCTTTCAGAGCCGTCATTTCCAGGCTGAGACTATTAATGCTACAGTGCCCAAGAC 832
 Db 326 ATACCTTTCAGAGCCGTCATTTCCAGGCTGAGACTATTAATGCTACAGTGCCCAAGAC 267
 QY 833 ATTAATTTATGGGATATGTCAAACACATTTGAAAGGTTTCTGTGAAATGATATCAAG 892
 Db 266 GTAATCCACTGGGATGTCAAACATCAATTTGAAAGGTTTCTGTGAAATGATATCAAA 207
 QY 893 GCTACACAAACCAACTTGAATGTTAAAGATTGACACCAATTTTACATAT 946
 Db 206 GATACACAAACCAACTTGAACGTAACTAACTAATTTACTTCTTTTACATAT 153

RESULT 15
 LOCUS BF212748 540 bp mRNA linear EST 06-NOV-2000
 DEFINITION 601813991F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048150 5',
 mRNA sequence.
 ACCESSION BF212748
 VERSION BF212748.1 GI:11106334
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
 Homidae; Homo.
 1 (bases 1 to 540)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
 http://image.llnl.gov
 Plate: LHC878 row: f column: 23
 High quality sequence stop: 540.
 Location/Qualifiers
 1..540
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4048150"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 54"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI
 (ggccatctggcc); Double-stranded cDNA was prepared from

FEATURES

source

1..540
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4048150"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 54"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI
 (ggccatctggcc); Double-stranded cDNA was prepared from

cellular line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTGGCC-3' and 3' adaptor sequence: 5'-ATTTCAGACGCCGACGGCGCCGACATG-dt (10) NH-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).¹⁰

ORIGIN

Query Match	11.1%;	Score 316.2;	DB 7;	Length 540;
Best Local Similarity	88.8%;	Pred. No. 7.2e-38;		
Matches 390; Conservative	0;	Mismatches 38;	Indels 11;	Gaps 4;

QY	1258	CCGAACTGGGGATTAAAAAGAAAGCTTATTTGTATTAATACCAAGTGGCTT--ATGAAAGTA	1316
Db	103	CTGAACACGGATTAAAGAAAGAGCTTTATGGTGAATACCAAGGGGCTTACATGAAGAT	162
QY	1317	TTCTTAATATGAAAAACAGCAATGTGTG-----AAATGCTACAGGAAAAATGTGAAC	1370
Db	163	ATTCTCTGATATAGAAAAACAGCAGTGTGTGTAAGTGTCTACAGGAAATATGTGAAC	222
QY	1371	TTATGAATTAATAAATTCGATGAGCAGGCTCTATATTTGTAATCCATGATTTACAGAGATA	1430
Db	223	TTATGAATTAATAAATTCGATGAGCAGGCTCTATATGTGTATCCATGATTTACAGAGATA	282
QY	1431	AAGAAATCTTCATCCCAAGAACAAAGCTTACAGACTACAAAGAGAGATACAGGACCC	1490
Db	283	AAGAAATCTTCATCCCAAGAACAAAGCTTACAGACTACAAAGAGAGATACAGGACCC	342
QY	1491	TGGAGACAAAGACTACCCGCAAACTCGTATTTCGACATATCTACAGTTGTATATTC	1556
Db	343	TGGAGACAAAGACTACCCGCAAACTCGTATTTCGACATATCTACAAAGTGTATATATTC	402
QY	1551	CTGATCTCAACACTGGATATATAAACCACAAATTTCTGTGCTGAGGGAAAGCCATC	1610
Db	403	CTGATCTCAACACTGGATATATAAACCACAAAGTCAAAATTCCTTG-CTAGGGGAAGCCATC	461
QY	1611	TCAGCAATTAATATGAAATTAATCTTCCTTAACAATTAA---CCACAGTTGATTCCTTAG	1667
Db	462	TCAGCAATTAATATGAAATTAATCTTCCTTAACAATTAAACAACACAGTTGTATTCCTTAG	521
QY	1668	ACTCAGGAAATTAATCCGAG	1686
Db	522	ACTCAGGAAATTAATCCGAG	540

Search completed: October 14, 2006, 16:18:17
Job time : 13055 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 12:13:19 ; Search time 1718 Seconds
(without alignments)
11602.828 Million cell updates/sec

Title: US-10-667-289-1

Perfect score: 2857.4
Sequence: 1 ggcgtacgggaattccatcgtc.....gtcctggaataaaaaaaa 2859

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: N_Geneseq_8:*
2: geneseqn1908:*
3: geneseqn1908:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2005a:*
15: geneseqn2005b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2857.4	100.0	2859	6	AAK98257
2	2857.4	100.0	2859	13	AD573604
3	2857.4	100.0	2859	14	AAE51089
4	2810.2	98.3	2830	6	AAAD8773
5	2081.4	72.8	2123	5	AAAF87820
6	1906	66.7	1910	5	AAAF87822
7	1887.6	66.1	1890	14	ADV43392
8	1493.6	52.3	1698	6	AAAD8774
9	1379	48.3	1887	6	AAAK8258
10	1326.6	46.3	1479	5	AAAF87819
11	1236.6	43.3	1301	5	AAAF87821
12	1140.6	39.9	1155	4	AAAC8149
13	1140.6	39.9	1155	10	ADCO7176
14	1140.6	39.9	1155	14	ADZ65011
15	1105.8	38.7	1935	6	AAAD8777
16	1043.4	36.5	1071	6	AAAD8775
17	1039.2	36.4	1784	5	AAAF87818
18	846.2	29.6	1152	4	AAAC8150

19	846.2	29.6	1152	10	ADC07178	Adc07178 Human DNA
20	846.2	29.6	1152	14	ADZ65013	Adz65013 Reverse t
21	254	8.9	36871	13	ABD33508	Abd33508 Human can
22	253.4	8.9	98844	7	ADJ84099	Adj84099 Human WRN
23	253.4	8.9	143776	13	ADV15288	Adv15288 Human ost
24	253.4	8.9	144034	13	ADV15294	Adv15294 Human ost
25	253	8.9	601	13	ADV15840	Adv15840 Human ost
26	248.6	8.7	31741	5	ABA21231	Ab21231 Human ner
27	248.6	8.7	44567	9	ADA02479	Ada02479 Human BAT
28	248.6	8.7	44567	9	ADA02479	Ada02479 Human BAT
29	248.6	8.7	44567	10	AD572218	Ad572218 Human BAT
30	248.4	8.7	212231	11	ACN44598	Acn44598 Human gen
31	248.2	8.7	270150	11	ADP65796	Adp65796 Human 16p
32	248	8.7	30652	14	AE894744	Ae894744 Human eif
33	247.8	8.7	8259	12	ADN41778	Adn41778 Novel hum
34	247.8	8.7	110000	14	ADP34666_1	Continuation (2 of
35	247.4	8.7	110000	10	AD570447_3	Continuation (4 of
36	247.4	8.7	110000	10	AB279565_3	Continuation (4 of
37	247	8.6	37262	11	ACN43890	Acn43890 Human gen
38	247	8.6	81001	4	AAF30035	AAF30035 Human apo
39	247	8.6	188971	12	ADL08108	Adl08108 Human gen
40	246.8	8.6	38732	14	ADL12821_4	Continuation (5 of
41	246.8	8.6	110000	14	ADL12821_3	Continuation (4 of
42	246.6	8.6	276276	11	ACN44350	Acn44350 Human gen
43	245.6	8.6	338702	11	ACN44042	Acn44042 Human gen
44	245.4	8.6	118067	12	ADP13110	Adp13110 Hypermeth
45	245.4	8.6	118067	12	ADJ37256	Adj37256 Hypermeth

ALIGNMENTS

RESULT 1	AAK98257	standard; cDNA; 2859 BP.
ID	AAK98257	
XX	AAK98257;	
AC		
XX		
DT	28-MAY-2002	(first entry)
XX		
DE	Human DNAX cytokine receptor subunit 5 (DCRS5) cDNA sequence.	
XX		
KM	Human; DNAX cytokine receptor subunit 5; DCRS5; IL30 receptor;	
KM	immune response; DCRS; p40/IL-830 ligand; cell physiology modulation;	
KM	cell development modulation; TH1-mediated disease; multiple sclerosis;	
KM	rheumatoid arthritis; psoriasis; sepsis; allogenic transplant; recipient;	
KM	diabetes; tumour; viral growth; fungal growth; vaccine;	
KM	TH2 response; tumour; viral growth; fungal growth; vaccine;	
KM	allergic response; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	119..2008
FT		/*tag= a
FT		/product= "DCRS5 protein"
FT		/transl_except= (pos:125..127, aa:Xaa)
FT		/note= "Xaa= Gln or His"
FT		/transl_except= (pos:563..545, aa:Xaa)
FT		/note= "Xaa= Arg or Gly"
FT	sig_peptide	119..187
FT		/*tag= b
FT	misc_feature	127
FT		/*tag= c
FT		/note= "If the base at this position is G (encoding Gln), the base at position 563 is also G (encoding Gly). If the base at this position is T (encoding His) the base at position 563 is A (encoding Arg)."
FT	mat_peptide	188..2005
FT		/*tag= d
FT		/note= "Mature DCRS5 protein"
FT	misc_feature	563
FT		/*tag= e

PT /note="If the base at this position is G (encoding Gly),
PT the base at position 127 is also G (encoding Gln). If the
PT base at this position is A (encoding Arg) the base at
PT position 127 is T (encoding His)"
XX
XX MO200185790-A2.
XX
XX 15-NOV-2001.
XX
XX 10-MAY-2001; 2001MO-US015057.
XX
XX 10-MAY-2000; 2000US-0203426P.
XX
XX (SCHE) SCHERING CORP.
XX
XX Chirica M, Kaetelein RA, Moore KW, Parham CL;
XX
XX MPI; 2002-062238/08.
XX
XX P-PSDB; AAO14008.
XX
XX Novel DNAX cytokine receptor subunit 5 polypeptide which is subunit of
PT receptor complex for p40/IL-830, useful for treating conditions
PT associated with abnormal expression or triggering of response to p40/IL-
PT 830 ligand.
XX
XX Claim 18; Page 9-12; 74bp; English.
XX
XX The present cDNA sequence encodes the human DNAX cytokine receptor
CC subunit 5 (defined as DCRS5 or IL30 receptor) of the invention. DCRS5 is
CC a member of the class I branch of the cytokine receptor superfamily and
CC is closely related to the IL-6 receptor subunit gp130 and the IL-12R-Beta
CC -2 subunit. Cytokines are soluble molecules which play a critical role in
CC controlling the complex cellular interactions of the immune response. The
CC invention comprises novel receptors related to cytokine receptors
CC designated DNAX cytokine receptor subunits (DCRS). Specifically the
CC invention comprises a subunit (DCRS5) for a receptor complex for the
CC p40/IL-830 ligand. The DCRS5 proteins of the invention are useful for
CC treating diseases or disorders associated with abnormal expression or
CC abnormal triggering of response to the p40/IL-830 ligand. The proteins of
CC the invention can be used to modulate the physiology or development of a
CC cell from a host which exhibits TH1-mediated disease; multiple sclerosis;
CC rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
CC diabetes; psoriasis; sepsis; an allogeneic transplant recipient; chronic
CC TH2 response; tumour; viral or fungal growth; vaccine recipient; or an
CC allergic response
XX
XX Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;
SQ
Query Match 100.0%; Score 2857.4; DB 6; Length 2859;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTAAGGGAATTTCCATTGTGTGGGACCAACAAAGGCTGGAGCTGGCTTGAAGT 60
DB 1 GTGGTAGGGAATTTCCATTGTGTGGGACCAACAAAGGCTGGAGCTGGCTTGAAGT 60
QY 61 GGAATTATGCTTCAACAGAGTTGAAAGAGGAAACAGCTTTTCTGCTTCAAGCAT 120
DB 61 GGAATTATGCTTCAACAGAGTTGAAAGAGGAAACAGCTTTTCTGCTTCAAGCAT 120
QY 121 GAATCAAGTCAATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 180
DB 121 GAATCAAGTCAATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 180
QY 121 GAATCAAGTCAATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 180
DB 121 GAATCAAGTCAATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 180
QY 181 TCATGAGAGAAATTAACAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 TCATGAGAGAAATTAACAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 TTTTAAGATGGGTATGAAATATCTCTATATATGTCGAAGAGCAATTAAGATGCAACC 300
DB 241 TTTTAAGATGGGTATGAAATATCTCTATATATGTCGAAGAGCAATTAAGATGCAACC 300
QY 301 AAGGAACTTCATTTTATATAAATGAGCATCAAGAAAGATTTCAATCAAGATTTAA 360

DB 301 AAGGAACTTCATTTTATATAAATGAGCATCAAGAAAGATTTCAATCAAGATTTAA 360
QY 361 TAAACACAGAGCTGGCTTGGATATAAACTTTGAGACCAATGCTTCTATGACTG 420
DB 361 TAAACACAGAGCTGGCTTGGATATAAACTTTGAGACCAATGCTTCTATGACTG 420
QY 421 CACTGCTGAATGTCCTCAACATTTTCAGAGACATGATATGAGAAAGACATTTCTTC 480
DB 421 CACTGCTGAATGTCCTCAACATTTTCAGAGACATGATATGAGAAAGACATTTCTTC 480
QY 481 TGGATATCCGCGCAGATATTCCTGATTAAGTAACTGTGCTATTAATATTCAGGCA 540
DB 481 TGGATATCCGCGCAGATATTCCTGATTAAGTAACTGTGCTATTAATATTCAGGCA 540
QY 541 CATGACTTGACCTGGAAATGCTGGAAGGCTCACTCATAGACACAAATACGTGTACA 600
DB 541 CATGACTTGACCTGGAAATGCTGGAAGGCTCACTCATAGACACAAATACGTGTACA 600
QY 601 TGTGAAGATTTAGAGACAGAAAGAGACAGATATCTCACTCAAGCTATATTAACAT 660
DB 601 TGTGAAGATTTAGAGACAGAAAGAGACAGATATCTCACTCAAGCTATATTAACAT 660
QY 661 CTCACATGATTCATTACAAAGGTGCAAGAAAGTACTTGTGGTCCAGACGAAACGC 720
DB 661 CTCACATGATTCATTACAAAGGTGCAAGAAAGTACTTGTGGTCCAGACGAAACGC 720
QY 721 ACTAGGCAATGGAAGATCAAAACAACTGCAAAATTCACCTGATATATGATACCTTC 780
DB 721 ACTAGGCAATGGAAGATCAAAACAACTGCAAAATTCACCTGATATATGATACCTTC 780
QY 781 TGGAGCTGATTCCTCAAGAGCTGAGACTATTAATGCTACAGTGCACAAACATAATTA 840
DB 781 TGGAGCTGATTCCTCAAGAGCTGAGACTATTAATGCTACAGTGCACAAACATAATTA 840
QY 841 TTGGGATGATCAAAACAACTTGAAGAGTTTCTGTGTAAGAGATAGAAAGCTCAAC 900
DB 841 TTGGGATGATCAAAACAACTTGAAGAGTTTCTGTGTAAGAGATAGAAAGCTCAAC 900
QY 901 AAACCAACCTGGAATGTTAAAGAAATTTGACACCAATTTTACATATGTCACACAGTCA 960
DB 901 AAACCAACCTGGAATGTTAAAGAAATTTGACACCAATTTTACATATGTCACACAGTCA 960
QY 961 ATTCTACTGAGACCAACATTAAGTACGATATTCAGTGAATGTCAGAAACAGGCAA 1020
DB 961 ATTCTACTGAGACCAACATTAAGTACGATATTCAGTGAATGTCAGAAACAGGCAA 1020
QY 1021 AAGGTACTGGACGCTTGGAGATTCACCGTTTTCATTAACACCTGAAACAGTCCCA 1080
DB 1021 AAGGTACTGGACGCTTGGAGATTCACCGTTTTCATTAACACCTGAAACAGTCCCA 1080
QY 1081 GGTCAATCAAAAGCATTTGCAACATACATACATACATACATACATACATACATACAT 1140
DB 1081 GGTCAATCAAAAGCATTTGCAACATACATACATACATACATACATACATACATACAT 1140
QY 1141 CTCACAGGACACCTTACTTCTGACAAAGAGACATTTGACATTTTATGGAATGAT 1200
DB 1141 CTCACAGGACACCTTACTTCTGACAAAGAGACATTTGACATTTTATGGAATGAT 1200
QY 1201 CGTCTTGTGCTTATGTTGATCAATTTCTTCTTGTGATTTGGAATTTTAACAGATTCGG 1260
DB 1201 CGTCTTGTGCTTATGTTGATCAATTTCTTCTTGTGATTTGGAATTTTAACAGATTCGG 1260
QY 1261 AACTGGGATTTAAAGAGATCTTATTTGTTAATACAAAGTGGCTTTATGAGATATTC 1320
DB 1261 AACTGGGATTTAAAGAGATCTTATTTGTTAATACAAAGTGGCTTTATGAGATATTC 1320
QY 1321 TAATATGAAACACAGCAATGTTGTGAAATGCTACAGAAATATAGTAACTTAATGAATA 1380
DB 1321 TAATATGAAACACAGCAATGTTGTGAAATGCTACAGAAATATAGTAACTTAATGAATA 1380
QY 1381 TAATTCAGTGAAGAGCTGCTATATGTTGATCCCATGATTAACAGATATAAGAAATCTT 1440

Db 1381 TAATTCAGTAGAGAGGTCCTATATGTTGATGCCAGATTAAGAGATTAAGAAATCTT 1440
 Qy 1441 CATCCAGAACACAGAGCTACAGACTACAGAGAGAGATACAGAGACCCCTGGAGACAG 1500
 Db 1441 CATCCAGAACACAGAGCTACAGACTACAGAGAGAGATTAAGAGACCCCTGGAGACAG 1500
 Qy 1501 AGACTACCCGCAAACTCGCTATTCGACAACTACTACAGTTGTATATATTCCTGATCTCAA 1560
 Db 1501 AGACTACCCGCAAACTCGCTATTCGACAACTACTACTACAGTTGTATATATTCCTGATCTCAA 1560
 Qy 1561 CATGGAATATAAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCTCAGCAATA 1620
 Db 1561 CATGGAATATAAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCTCAGCAATA 1620
 Qy 1621 TAATGAATAATTAATCTCTTAACCTTAACCAAGTATTCCTTACAGTACAGGAATA 1680
 Db 1621 TAATGAATAATTAATCTCTTAACCTTAACCAAGTATTCCTTACAGTACAGGAATA 1680
 Qy 1681 TCCAGAGTTACAAAAGCATCTTAATTTTGTCTTTTCTGTTTCAAGTGTGAATTCAGT 1740
 Db 1681 TCCAGAGTTACAAAAGCATCTTAATTTTGTCTTTTCTGTTTCAAGTGTGAATTCAGT 1740
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 Db 1741 CAACACATATTTCTTGGAGATTTAGCCTCATATTAATCAAGAGAGATTCAGTTCTCC 1800
 Qy 1801 TGACATCAAACTCAGTAGAGAGGAGAAACACACATCTTTGGAAATGATTCACCCAG 1860
 Db 1801 TGACATCAAACTCAGTAGAGAGGAGAAACACACATCTTTGGAAATGATTCACCCAG 1860
 Qy 1861 TGAATCTATTCAGAACAGACCCCTGCTTCCGTGATGAATTTGCTCTGTTGGGGATCGT 1920
 Db 1861 TGAATCTATTCAGAACAGACCCCTGCTTCCGTGATGAATTTGCTCTGTTGGGGATCGT 1920
 Qy 1921 GAATGAGAGAGTCCCATCTATTAATACTTAATTTTCCCAAAATATTTTGGAAAGCCACTT 1980
 Db 1921 GAATGAGAGAGTCCCATCTATTAATACTTAATTTTCCCAAAATATTTTGGAAAGCCACTT 1980
 Qy 1981 CAATAGAGATTTCACTCTGAGAAAGTAGAGCTGTGTGTGTAATTAATGAGAAAGCT 2040
 Db 1981 CAATAGAGATTTCACTCTGAGAAAGTAGAGCTGTGTGTGTAATTAATGAGAAAGCT 2040
 Qy 2041 GCCTTCGAATCTGAACCTTGGGTTTCCCTGCAATAGAAATTTGAATTCGCTCTTTTGA 2100
 Db 2041 GCCTTCGAATCTGAACCTTGGGTTTCCCTGCAATAGAAATTTGAATTCGCTCTTTTGA 2100
 Qy 2101 AAAAAATGATTCACATACAAATCTTCACATGACACATGTTTCAATTCCTTGGATTA 2160
 Db 2101 AAAAAATGATTCACATACAAATCTTCACATGACACATGTTTCAATTCCTTGGATTA 2160
 Qy 2161 ATACCTAGTAGAGGAGTGTGTGGGCCATAGATAGAGATATGTTTCAGTTCTACCAATCT 2220
 Db 2161 ATACCTAGTAGAGGAGTGTGTGGGCCATAGATAGAGATATGTTTCAGTTCTACCAATCT 2220
 Qy 2221 TGTTCACAGAGTAGATCTTTCTGTGCTCTACATCAACATGTAAGATTTCCCGGAG 2280
 Db 2221 TGTTCACAGAGTAGATCTTTCTGTGCTCTACATCAACATGTAAGATTTCCCGGAG 2280
 Qy 2281 CTCATAGCTTTTAAATTTTAAAGCATTCTTCTGCTTAATTTCTTAAATTAAGAAATTA 2340
 Db 2281 CTCATAGCTTTTAAATTTTAAAGCATTCTTCTGCTTAATTTCTTAAATTAAGAAATTA 2340
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 Db 2341 GGTCCGAGAGTAGAGACATGCTTCATGTGTACACATACAGGACCAAAAAACAGCATTTATGT 2400
 Qy 2401 GAGAGCTCATGATTTTATATAGAGTCACTATTTCTCTTATTTTCCCTCATTTGAAA 2460
 Db 2401 GAGAGCTCATGATTTTATATAGAGTCACTATTTCTCTTATTTTCCCTCATTTGAAA 2460
 Qy 2461 GATGCAAAACAGCTCTCTATTTGTGTACAGAAAGGTTAAATATGCAAAATATCCTGTAGT 2520
 Db 2461 GATGCAAAACAGCTCTCTATTTGTGTACAGAAAGGTTAAATATGCAAAATATCCTGTAGT 2520

Qy 2521 AAAATAAATGCTGAAAATTTTCTTTAAATAGAAATCATTAGGCCAGGCGTGTGCTCA 2580
 Db 2521 AAAATAAATGCTGAAAATTTTCTTTAAATAGAAATCATTAGGCCAGGCGTGTGCTCA 2580
 Qy 2581 TGCCTTGAATCCAGACATTTGTGTAGGCTGTAGGTGTGTGTATCACTGAGTCAAGAGTT 2640
 Db 2581 TGCCTTGAATCCAGACATTTGTGTAGGCTGTAGGTGTGTGTATCACTGAGTCAAGAGTT 2640
 Qy 2641 CGAGTCCAGCTTGGCCAAATATGCTGAATCCCTGTCTCTACTAATAATTAACAAAATTAGCC 2700
 Db 2641 CGAGTCCAGCTTGGCCAAATATGCTGAATCCCTGTCTCTACTAATAATTAACAAAATTAGCC 2700
 Qy 2701 GGGCATGTGTGGAGGTGTGTATATCCAGCTACTTGGAGGCTGTAGGAGAGAAATCAC 2760
 Db 2701 GGGCATGTGTGGAGGTGTGTATATCCAGCTACTTGGAGGCTGTAGGAGAGAAATCAC 2760
 Qy 2761 TTGAACCAAGAGAGAGAGGTGTGCACTGAGCTGAGATTTGTGCCACTGCACTCCAGCCTGG 2820
 Db 2761 TTGAACCAAGAGAGAGAGGTGTGCACTGAGCTGAGATTTGTGTGCCACTGCACTCCAGCCTGG 2820
 Qy 2821 GCAACAGAGCAAACTCTGTCTGTGAAAAAATTTTAAAAA 2859
 Db 2821 GCAACAGAGCAAACTCTGTCTGTGAAAAAATTTTAAAAA 2859
 RESULT 2
 ADS73604
 ID ADS73604 standard; cDNA; 2859 BP.
 XX
 AC ADS73604;
 XX
 AC
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human IL-23r coding sequence.
 XX
 KW se; gene; human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour;
 KW growth; agonist; antagonist; receptor; cancer; antigen-binding site;
 KW antibody; extracellular region; antisense nucleic acid;
 KW small interference RNA; siRNA; polyclonal; monoclonal; humanized; Fab;
 KW Fv; F(ab')2; peptide mimetic; colon; ovarian; breast; melanoma; cachexia;
 KW anorexia; angiogenesis; gastrointestinal tract; respiratory tract;
 KW reproductive system; endocrine system.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 119..2008
 FT /tag= b
 FT /product= "IL-23r"
 FT sig_peptide 119..187
 FT /tag= a
 FT mat_peptide 188..2005
 FT /tag= c
 XX
 PN MO2004081190-A2.
 XX
 PD 23-SEP-2004.
 XX
 PF 09-MAR-2004; 2004MO-US007198.
 XX
 PR 10-MAR-2003; 2003US-0453672P.
 XX
 PA (SCHE) SCHERRING CORP.
 XX
 PI Ofc M, Mcclanahan TK;
 XX
 XX WPI: 2004-668951/65.
 DR P-PSDB; ADS73605.
 XX
 PT Modulating tumor growth, useful for treating a subject suffering from
 PT cancer or tumor, comprises contacting a tumor cell with an agonist or
 PT antagonist of IL-23.

XX Claim 4; SEQ ID NO 5; 57pp; English.

XX This sequence encodes human interleukin 23 receptor (IL-23R). The method
XX the invention for modulating tumour growth comprises contacting a
XX tumour cell with an agonist or antagonist of IL-23. The agonist or
XX antagonist is a binding composition which specifically binds the IL-23
XX p19 subunit (IL-23p19) or the IL-23R protein. The identified agonist or
XX antagonist may be used for diagnosing or treating a subject suffering
XX from a cancer or tumour. The binding composition comprises an antigen-
XX binding site of the antibody, an extracellular region of IL-23R, a small
XX molecule, an antisense nucleic acid or small interference RNA (siRNA), or
XX a detectable label. The binding composition comprises a polyclonal
XX antibody, a monoclonal antibody, a humanized antibody or its fragment, a
XX Fab, Fv, F(ab')₂ fragment, or a peptide mimetic of an antibody. The
XX tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell.
XX In the treatment method, the antagonist of IL-23 inhibits growth of
XX cancer or tumour, cachexia, anorexia or angiogenesis. The cancer or
XX tumour is of the gastrointestinal tract, respiratory tract, reproductive
XX system or endocrine system. In diagnosing cancer or tumour, the binding
XX composition comprises a nucleic acid probe or primer that specifically
XX binds or hybridizes to human or mouse IL-23p19 cDNA sequences, or the
XX human IL-23R sequence.

XX Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;

XX Query Match 100.0%; Score 2857.4; DB 13; Length 2859;

XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGTACGGGAATTCATTGTGTGGGACCAAGGCTGGACCTGGCTTGAAGT 60
DB 1 GTGGTACGGGAATTCATTGTGTGGGACCAAGGCTGGACCTGGCTTGAAGT 60
QY 61 GGAATTATGCTTCAACAGGTTGAAAGAGGGAACAGCTTTCTCTCCAGCAT 120
DB 61 GGAATTATGCTTCAACAGGTTGAAAGAGGGAACAGCTTTCTCTCCAGCAT 120
QY 121 GAATCAAGTCACTATTCATGAGATGAGATAGCCCTTATACATCTCTCAGCTGG 180
DB 121 GAATCAAGTCACTATTCATGAGATGAGATAGCCCTTATACATCTCTCAGCTGG 180
QY 181 TCATGAGAGATTAACAATATTAATCTGCTGGCCACATCTGGGTAGAACCCACAAT 240
DB 181 TCATGAGAGATTAACAATATTAATCTGCTGGCCACATCTGGGTAGAACCCACAAT 240
QY 241 TTTTAAAGATGGATGATGATATCTCTATATATGCGAAGCAAGCAATTAGAACCTGCAACC 300
DB 241 TTTTAAAGATGGATGATGATATCTCTATATATGCGAAGCAAGCAATTAGAACCTGCAACC 300
QY 301 AAGGAACCTCATTTTATATAAATGAGCATCAAGAAAGATTTCAATCAACAGATTAA 360
DB 301 AAGGAACCTCATTTTATATAAATGAGCATCAAGAAAGATTTCAATCAACAGATTAA 360
QY 361 TAAACCAACGCTGGCTTTGATATAAACTTTCTGAAACCAATGCTTCTATGATCTG 420
DB 361 TAAACCAACGCTGGCTTTGATATAAACTTTCTGAAACCAATGCTTCTATGATCTG 420
QY 421 CACTGCGAATGTCCTCCAAACATTTTCAAGAGACCTGATATGAGAAAGACATTTCTTC 480
DB 421 CACTGCGAATGTCCTCCAAACATTTTCAAGAGACCTGATATGAGAAAGACATTTCTTC 480
QY 481 TGAATATCCGCGAGATATTCCTGATGAGATTAACCTGTGTCACTTATGAAATATTCAGGCAA 540
DB 481 TGAATATCCGCGAGATATTCCTGATGAGATTAACCTGTGTCACTTATGAAATATTCAGGCAA 540
QY 541 CATGACTTGCACTGGATGCTGGAAGCTGACCTATACATAGACCAAAATACGCTGATCA 600
DB 541 CATGACTTGCACTGGATGCTGGAAGCTGACCTATACATAGACCAAAATACGCTGATCA 600
QY 601 TGTGAAGAGTTTGAAGACAGAAAGAGCAACAGTATCTCACTCAAGCTATATTAACAT 660
DB 601 TGTGAAGAGTTTGAAGACAGAAAGAGCAACAGTATCTCACTCAAGCTATATTAACAT 660

QY 661 CTCACATGATTCATTAACAAGGTGGCAAGAGTACTTGTGTTGGCTCCAAAGCAAAACGC 720
DB 661 CTCACATGATTCATTAACAAGGTGGCAAGAGTACTTGTGTTGGCTCCAAAGCAAAACGC 720
QY 721 ACTAGGCAATGGAAGGTCAAAACAATGCAATTTCACTGGATGATATGATTAACCTTC 780
DB 721 ACTAGGCAATGGAAGGTCAAAACAATGCAATTTCACTGGATGATATGATTAACCTTC 780
QY 781 TGCAGCGTCAATTTCCAGGGCTGAGACTATTAATGCTACAGTGCACCAACATAATTTA 840
DB 781 TGCAGCGTCAATTTCCAGGGCTGAGACTATTAATGCTACAGTGCACCAACATAATTTA 840
QY 841 TTGGATATGCTCAACCAACATTTGAAAAGTTCTGTGAAATGAGATTAACAGCTCAAC 900
DB 841 TTGGATATGCTCAACCAACATTTGAAAAGTTCTGTGAAATGAGATTAACAGCTCAAC 900
QY 901 AAACCAACTGGGAATGTTAAAGAAATTTGACCAATTTTACATATGTCACACAGTCAGA 960
DB 901 AAACCAACTGGGAATGTTAAAGAAATTTGACCAATTTTACATATGTCACACAGTCAGA 960
QY 961 ATTCTACTTGAGCCCAACATTAAGTACGATATTTCAAGTGAATGTCAAGAAACAGGCAA 1020
DB 961 ATTCTACTTGAGCCCAACATTAAGTACGATATTTCAAGTGAATGTCAAGAAACAGGCAA 1020
QY 1021 AAGGTACTGGACGCTTGGAGTTACCGTTTTCATTAACAACCTGGAACAGTTCCCA 1080
DB 1021 AAGGTACTGGACGCTTGGAGTTACCGTTTTCATTAACAACCTGGAACAGTTCCCA 1080
QY 1081 GGTCAATCAAAAAGCATTCACATGACACATGGAATTCGAGGCTAACAGTTGCTTCAT 1140
DB 1081 GGTCAATCAAAAAGCATTCACATGACACATGGAATTCGAGGCTAACAGTTGCTTCAT 1140
QY 1141 CTCTACAGGCGCACTTACTTGTGACCAACAGAGAGACATTTGACATTTTATTTGGAATGAT 1200
DB 1141 CTCTACAGGCGCACTTACTTGTGACCAACAGAGAGACATTTGACATTTTATTTGGAATGAT 1200
QY 1201 CGTCTTGTGCTTATGTTGTCATTTCTTTCTTTGATGGATATTTTACAGATCATTTCCG 1260
DB 1201 CGTCTTGTGCTTATGTTGTCATTTCTTTCTTTGATGGATATTTTACAGATCATTTCCG 1260
QY 1261 AACTGGATTTAAAGAAAGATCTTATTTGTAATACAAAGTGGCTTTATGAAATATTC 1320
DB 1261 AACTGGATTTAAAGAAAGATCTTATTTGTAATACAAAGTGGCTTTATGAAATATTC 1320
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DB 1321 TAATATGAAAACAGCAATGTTGTGAAAATGCTACAGAAATATGTAACCTTATGAAATTA 1380
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DB 1381 TAAATTCAGTGAAGCAGTCTTATATGTTGATCCCATGATTAACAGATTAAGAAATCTT 1440
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DB 1441 CATCCGAGAACCAACCTTACAGATTAACAGAAAGAAATACAGAACCTCTGAGACAG 1500
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DB 1501 AGACTACCGGCAAACTGCTATTTGCAACAATCAAGTTGTAATATTCCTGATCTCAA 1560
QY 1561 CACTGATATTAACCCCAAAATTTCAATTTTCTGCTGAGAGGAAGCACTTCAGCAATTA 1620
DB 1561 CACTGATATTAACCCCAAAATTTCAATTTTCTGCTGAGAGGAAGCACTTCAGCAATTA 1620
QY 1621 TAATGAAATTAATCTCTTAAACCTTAAACCAACAGTTGATTCCTTGAAGTCAAGAAATTA 1680
DB 1621 TAATGAAATTAATCTCTTAAACCTTAAACCAACAGTTGATTCCTTGAAGTCAAGAAATTA 1680
QY 1681 TCCAGGTTACAAAGACATCTAATTTGCTTTTCTGTTTCAAGTGTGAATTCATAAG 1740
DB 1681 TCCAGGTTACAAAGACATCTAATTTTCTTTTCTGTTTCAAGTGTGAATTCATAAG 1740

QY	1741	CAACAAATATTTCTGAGAAATTAAAGCTCAATTTAAATGAGAGAAATGACATTCCTC	1800
Db	1741	CAACCAATATTTCTTGAGAAATTAAAGCTCAATTTAAATCAGAGAAATGACATTCCTC	1800
QY	1801	TGACATACAAAACTCAGTAGAGAGAGAAACAACCATGCTTTTGAAAAATGATTCACCCAG	1860
Db	1801	TGACATACAAAACTCAGTAGAGAGAGAAACAACCATGCTTTTGAAAAATGATTCACCCAG	1860
QY	1861	TGAAACTATTCAGAACAGACCCTGCTTCGTAGTAATTTGTCTCTGTGTTGGGGATCGT	1920
Db	1861	TGAAACTATTCAGAACAGACCCTGCTTCGTAGTAATTTGTCTCTGTGTTGGGGATCGT	1920
QY	1921	GAATGAGAGATTCGCATCTATTTAACTTATTTTCCAAAAATTTTGGAAAGCCACTT	1980
Db	1921	GAATGAGAGATTCGCATCTATTTAACTTATTTTCCAAAAATTTTGGAAAGCCACTT	1980
QY	1981	CAATAGCATTTCACTCTTGAAAAAGTAGAGCTGTGCTCAAAATTCATAGAGAAAGCT	2040
Db	1981	CAATAGCATTTCACTCTTGAAAAAGTAGAGCTGTGCTCAAAATTCATAGAGAAAGCT	2040
QY	2041	GCCTTGCATCTGAACTTGGGTGTTTCCCTGCATATAGAAATGAAATTCGCTCTTTTGA	2100
Db	2041	GCCTTGCATCTGAACTTGGGTGTTTCCCTGCATATAGAAATGAAATTCGCTCTTTTGA	2100
QY	2101	AAAAAATGATTCACATACAAATCTTCACATGACACATGTTTCATTTCCCTTGATAA	2160
Db	2101	AAAAAATGATTCACATACAAATCTTCACATGACACATGTTTCATTTCCCTTGATAA	2160
QY	2161	ATACCTAGGTAGGGATTTGCTGGGCGAATAGATAGCATAGTTTCAGTTCTACCAATCT	2220
Db	2161	ATACCTAGGTAGGGATTTGCTGGGCGAATAGATAGCATAGTTTCAGTTCTACCAATCT	2220
QY	2221	TGTTTCCAGATGATGACATTTCTGTGCTCCACATCACCATGATAGAAATTCGCCGGAG	2280
Db	2221	TGTTTCCAGATGATGACATTTCTGTGCTCCACATCACCATGATAGAAATTCGCCGGAG	2280
QY	2281	CTCCATGCTTTTAAATTTTAGCCATTCCTGTGCCCTMAATTTCTTAAATTAGAAATTTA	2340
Db	2281	CTCCATGCTTTTAAATTTTAGCCATTCCTGTGCCCTMAATTTCTTAAATTAGAAATTTA	2340
QY	2341	GGTCCCGAAGGTGGAAACATGCTTCATGCTCACATACAGGCAAAAAACGCAATTAATGT	2400
Db	2341	GGTCCCGAAGGTGGAAACATGCTTCATGCTCACATACAGGCAAAAAACGCAATTAATGT	2400
QY	2401	GAGCGCTCAATGATATTTTATTAAGAGTCAAATATTCCTCTTTATTTTCCCTCAATTGAA	2460
Db	2401	GAGCGCTCAATGATATTTTATTAAGAGTCAAATATTCCTCTTTATTTTCCCTCAATTGAA	2460
QY	2461	GATGCAAAACAGCTCTCTATTTGTGTACAGAAAGGGTAAATATATGCAAAATACCTGTAGT	2520
Db	2461	GATGCAAAACAGCTCTCTATTTGTGTACAGAAAGGGTAAATATATGCAAAATACCTGTAGT	2520
QY	2521	AAAAATAAATGCTGAAAAATTTTCTTTAAATAATGATCAATGAGGCGAGGCTGTGCTCA	2580
Db	2521	AAAAATAAATGCTGAAAAATTTTCTTTAAATAATGATCAATGAGGCGAGGCTGTGCTCA	2580
QY	2581	TGCTTTGTAATCCACAGCACTTTGGTAGAGGTGAGGTGATCACTGAGGCTCAGAGATT	2640
Db	2581	TGCTTTGTAATCCACAGCACTTTGGTAGAGGTGAGGTGATCACTGAGGCTCAGAGATT	2640
QY	2641	CGAGTCCAGCTGGCCAAATATGCTGAAACCCCTGTCTCTACTTAAATTTACAAAAATTAGCC	2700
Db	2641	CGAGTCCAGCTGGCCAAATATGCTGAAACCCCTGTCTCTACTTAAATTTAGCC	2700
QY	2701	GGCCATGGTGGCAGGTGCTTGTAAATCCACGCTACTTTGGAGGCTGAGGCAAGAAATCAC	2760
Db	2701	GGCCATGGTGGCAGGTGCTTGTAAATCCACGCTACTTTGGAGGCTGAGGCAAGAAATCAC	2760
QY	2761	TTGAACCAAGAGAGGAGAGGTTTGACATGAGCTGAGATTGTGTCACTGCACTTCAGCCTGG	2820
Db	2761	TTGAACCAAGAGAGGAGAGGTTTGACATGAGCTGAGATTGTGTCACTGCACTTCAGCCTGG	2820
QY	2821	GCAACAGAGCAAACTCTGTCTGCAAAAAAATTTTAAAAA 2859	

Db	Accession	Score	Length	Query Match
2821	GCACAGACCAACTCTGTCTGGAAAAAAAAAAAAAAAA	100.0%	2859	2859
RESULT 3				
AEAS1089				
ID	AEAS1089 standard; DNA; 2859 BP.			
XX	AEAS1089;			
AC				
XX				
XX	11-AUG-2005 (first entry)			
DT				
XX				
XX	Human DNAX cytokine receptor subunit 5 (DCRS5) DNA.			
DE				
XX	Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder;			
KW	inflammation; respiratory disease; allergy; anti-allergic;			
KW	chronic obstructive pulmonary disease; respiratory-gen.;			
KW	pulmonary fibrosis; antiinflammatory; pneumonia; infection;			
KW	cytokine receptor family; gene; ds.			
XX				
XX	Homo sapiens.			
OS				
XX				
PH	Key	Location/Qualifiers		
FT	sig_peptide	1..187		
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FT		119..2008		
FT	CDS	/*tag= b		
FT		/product= "Human DNAX cytokine receptor subunit 5 (DCRS5		
FT		protein"		
FT		/transl_except= (pos:125..127, aa: Xaa)		
FT		/note= "Xaa corresponds to Gln or His"		
FT		/transl_except= (pos:563..565, aa: Xaa)		
FT		/note= "Xaa corresponds to Gly or Arg"		
FT	mat_peptide	188..2005		
FT		/*tag= c		
FT		/product= "Mature human DNAX cytokine receptor subunit 5		
FT		(DCRS5) protein"		
XX				
XX	WO2005052157-A1.			
XX				
XX	09-JUN-2005.			
PD				
XX				
XX	18-NOV-2004; 2004WO-US038886.			
PF				
PR	21-NOV-2003; 2003US-00720206.			
XX				
XX	(SCHE) SCHERING CORP.			
PA				
XX	Chirica M, Kaestlein RA, Moore KW, Parham CL;			
PI				
XX	WPI: 2005-418000/42.			
DR	P-PSDB; AEAS1090.			
XX				
XX				
PT	Use of an agonist or antagonist of DNAX cytokine receptor subunit 5			
PT	(DCRS5) or of p19 for treating a human subject experiencing a			
PT	physiological disorder such as allergy or chronic obstructive pulmonary			
PT	disorder (COPD).			
XX				
XX	Claim 1; SEQ ID NO 1; 89pp; English.			
XX				
XX	The present invention relates to a method of treating a human subject			
XX	experiencing a physiological disorder. The method involves administering			
CC	an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5), also			
CC	known as IL-23r) or of p19, where the disorder comprises asthma or			
CC	allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial			
CC	lung disorder. The invention is useful for treating interstitial lung			
CC	disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and			
CC	hypersensitivity pneumonitis. The present sequence is the human DCRS5			
CC	DNA.			
XX				
XX	Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;			
SO				

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGTACGGGAATTCATGTGTGGGACGCAACAGGGGAGCGCTGGCTGAAGT 60
Db 1 GTGGTACGGGAATTCATGTGTGGGACGCAACAGGGGAGCGCTGGCTGAAGT 60
QY 61 GGAATTATGTCTTCAACACAGGTTGAAAGAGGAAACAGTCTTTCCTGCTTCAAGCAT 120
Db 61 GGAATTATGTCTTCAACACAGGTTGAAAGAGGAAACAGTCTTTCCTGCTTCAAGCAT 120
QY 121 GAATCAAGTCACTTATTAATGGGATGCGATTAATGCGCTTTACATATCTTCAAGCTGCTG 180
Db 121 GAATCAAGTCACTTATTAATGGGATGCGATTAATGCGCTTTACATATCTTCAAGCTGCTG 180
QY 181 TCAATGAGGAATTAACAAATATTAACGCTGCTGGGACATCATGGGTAGAACAGCCACAAT 240
Db 181 TCAATGAGGAATTAACAAATATTAACGCTGCTGGGACATCATGGGTAGAACAGCCACAAT 240
QY 241 TTTTAAGATGGGATATGAATATCTCTATATATTTGGCAAGACAAATTAAGAACTGCCAAC 300
Db 241 TTTTAAGATGGGATATGAATATCTCTATATATTTGGCAAGACAAATTAAGAACTGCCAAC 300
QY 301 AAGGAAATCTCATTTTATATATAAATGGCATCAAAAGAAAGATTCAAAATCAAGAGATTAA 360
Db 301 AAGGAAATCTCATTTTATATATAAATGGCATCAAAAGAAAGATTCAAAATCAAGAGATTAA 360
QY 361 TAAAGCAACAGCTCGGCTTTGGTATTAATAAATCTTCTGGAAACCAATGCTCTATATGTA 420
Db 361 TAAAGCAACAGCTCGGCTTTGGTATTAATAAATCTTCTGGAAACCAATGCTCTATATGTA 420
QY 421 CACTGCTGAATGTCCCAACATTTTCAAGAGACACTATATGTGAAAGAAAGACATTTCTTC 480
Db 421 CACTGCTGAATGTCCCAACATTTTCAAGAGACACTATATGTGAAAGAAAGACATTTCTTC 480
QY 481 TGAATATCCGCCAGATATTCCTGATGAAGTAACCTGTGTCAATTTATGAATATTCAGGCAA 540
Db 481 TGAATATCCGCCAGATATTCCTGATGAAGTAACCTGTGTCAATTTATGAATATTCAGGCAA 540
QY 541 CAGGACTTGAACCTGGATGCTGGAAGCTCACTCATATGACCAAAATACGGGTGACA 600
Db 541 CAGGACTTGAACCTGGATGCTGGAAGCTCACTCATATGACCAAAATACGGGTGACA 600
QY 601 TGTGAAGAGTTTAAAGACAGAGAAAGACAAACAGTATCTCACTCAAGCTATATTAACAT 660
Db 601 TGTGAAGAGTTTAAAGACAGAGAAAGACAAACAGTATCTCACTCAAGCTATATTAACAT 660
QY 661 CTCACCTGATTCATTACAAAGGTGCAAGAAAGTACTTGTTGGGTCCAAAGCAAGCAACGC 720
Db 661 CTCACCTGATTCATTACAAAGGTGCAAGAAAGTACTTGTTGGGTCCAAAGCAAGCAACGC 720
QY 721 ACTATGAGCATGGAAGAGTCAAAACAACTGCAATTCACCTGATATATGATACCTTC 780
Db 721 ACTATGAGCATGGAAGAGTCAAAACAACTGCAATTCACCTGATATATGATACCTTC 780
QY 781 TGCAGCGGTCAATTCAGAGGCTGAGACTATTAATGCTACAGTCCCAAGACATTAATTTA 840
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Db 841 TTGGGATAGTCAACAACTTGAAGAGTTTCTGTGAATGAGATACAAAGGCTTACAC 900
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 DB 2581 TGTCTTGAATCCAGCATTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
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 DB 2821 GCAACAAAGAGCAAACTCTGTCTGGAATAAAAAAAAAAAAAA 2859
 RESULT 4
 AAD38773
 ID AAD38773 standard; CDNA; 2830 BP.
 AC AAD38773;
 XX 23-SEP-2002 (first entry)
 DT
 DE Human haematopoietin receptor 2 (HPR2) CDNA.
 XX
 KM Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
 KM pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 KM neurodegenerative disorder; leukemia; carcinoma; haematologic disorder;
 KM cancer; myeloid/lymphoid syndrome; idiopathic thrombocytopenic purpura;
 KM IRP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KM osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
 KM anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KM demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KM stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KM ischaemic disease; gene; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 107..1996
 FT CDS
 FT /+tag= a
 FT /product= "Human HPR2 protein"
 FT /note= "This region is specifically claimed as SEQ ID NO:
 FT 20 in claim 9 of the specification"
 FT sig_peptide
 FT 137..175
 FT /+tag= b
 FT mat_peptide
 FT 176..1993
 FT /+tag= c
 FT /product= "Human mature HPR2 protein"
 FT variation
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 FT variation
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 FT /replace(2172, G)
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 PN WC0200229060-A2.
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 PD 11-APR-2002.
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 PF 05-OCT-2001; 2001MO-US031634.
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 PR 13-OCT-2000; 2000US-0240476P.
 PR 20-FEB-2001; 2001US-0270282P.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 DR WPI: 2002-330172/36.
 DR P-PSDB; AAE24033.
 XX
 PT Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions.
 XX
 PS Claim 9; Page 117-119; 136pp; English.
 XX
 CC The present invention relates to human and murine haematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various haematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as
 CC osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence is
 CC human HPR1 CDNA

SQ Sequence 2830 BP; 922 A; 574 C; 551 G; 783 T; 0 U; 0 Other;
Query Match 98.3%; Score 2810.2; DB 6; Length 2830;
Best local Similarity 99.8%; Pred. No. 0;
Matches 2809; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 148 AGTAATAGCCTTTACATACCTTTCAGCTGTGTGATGAGAAATTACAAATATTAACCTG 207
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QY 208 CTCTGGCCACATCTGGGTAGAACCCAGCACAAATTTTTAAGATGGGTATGAAATCTCTAT 267
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DB 1156 CAGAGGACATTTGACTTTTATTTGGGAATGATCGTCTTTCCTGTTATGTGCAATTC 1215
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DB 1576 TTTTTCCTGAGGAAGCCATCTCAGCAATTAATTAAGAAATTAATCTTCTTAACTTAA 1635
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DB 1636 AACCAAGTTGATTTCTTACAGCAATTAATCCAGGTTACAAAGCAATCTTAATTT 1695
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DB 1696 TGCCTTTTCTGTTCAAGTGTGAATCACTAAGCAACAATATTTCTTGGAAATTTAAG 1755
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QY 1948 TTAATTTTCAAAAATATTTTGGAAAAGCACTTCAATAGATTTCACTTGGAAAAGTA 2007
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Qy	2728	CAGCTACTTGGGAGGCTGAGGCGAGAGATCACTTGAACAGGAAGCGAGAGTGTGCACT	2787
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Qy	2788	GAGCTGAAGTTGTGCCCACTGCATCTCCAGCTCTGGGCAACMAAGCAAAATCTGTGTC	2842
Db	2776	GAGCTGAAGTTGTGCCCACTGCATCTCCAGCTCTGGGCAACMAAGCAAAATCTGTGTC	2830

RESULT	5
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ID	AAF87820 standard; cDNA; 2123 BP.
XX	
AC	AAF87820;
XX	
DT	11-JUL-2001 (first entry)
XX	
DE	Human haemopoietin receptor protein NR12.3 encoding cDNA SEQ ID NO:5
XX	
KW	Human; haemopoietin receptor protein; NR12; immunosuppressive; antiallergic; haemopoietin factor; autoimmune disease; tissue reject metal allergy; pollen allergy; se.
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XX	
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XX	

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Qy      1348 AATGCTACAGGAAATATGTAATTTATGATATTAATTTCCAGTGAAGAGTCTTATATGT 1407
Db      1327 AATGCTACAGGAAATATGTAATTTATGATATTAATTTCCAGTGAAGAGTCTTATATGT 1386
Qy      1408 TGATCCCATATTTACAGAGATTAAGAAATCTTCATCCGAAACACAAGGCTACAGACTA 1467
Db      1387 TGATCCCATATTTACAGAGATTAAGAAATCTTCATCCGAAACACAAGGCTACAGACTA 1446
Qy      1468 CAAAGAGGAATTAACAGACCCCTGAGACAAAGACTACCCGCAAAATCGCTATTGCA 1527
Db      1447 CAAAGAGGAATTAACAGACCCCTGAGACAAAGACTACCCGCAAAATCGCTATTGCA 1506
Qy      1528 CAATACTACAGTGTATATATTCCTGATCTCAACACTGATATTAACCCCAATTTCAA 1587
Db      1507 CAATACTACAGTGTATATATTCCTGATCTCAACACTGATATTAACCCCAATTTCAA 1566
Qy      1588 TTTTTCGCGGAGGAGGACATCGACCAATTAATTAAGAAATTAATCTCTTAACACTTA 1647
Db      1567 TTTTTCGCGGAGGAGGACATCGACCAATTAATTAAGAAATTAATCTCTTAACACTTA 1626
Qy      1648 ACCACAGTGAATCTCTTAGACTCAGAAATTAATCCAGGTTACAAAGACATCTAATTT 1707
Db      1627 ACCACAGTGAATCTCTTAGACTCAGAAATTAATCCAGGTTACAAAGACATCTAATTT 1686
Qy      1708 TGCCTTTTCTGTTCAAGTGTGAATTCATGAGACACAAATATTTCTTGAGAAATTAAG 1767

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Db      1687 TGCCTTTTCTGTTCAAGTGTGAATTCATTAAGCAACAAATATTTCTTGAGAAATTAAG 1746
Qy      1768 CTTCAATATTAATCAAGAGAAATGCAATTCCTGACATACAAAACTCAAGTAGAGAGGA 1827
Db      1747 CTTCAATATTAATCAAGAGAAATGCAATTCCTGACATACAAAACTCAAGTAGAGAGGA 1806
Qy      1828 AACCAACATGCTTTTGGAAATATGATTCACCGAGTGAACATATTCAGAAACAGACCTTGCT 1887
Db      1807 AACCAACATGCTTTTGGAAATATGATTCACCGAGTGAACATATTCAGAAACAGACCTTGCT 1866
Qy      1888 TCCGTGATGAATTTGTCCTCCGTTTGGGGATTCGTGAATGAGAGAGTTGCAATTAATAC 1947
Db      1867 TCCGTGATGAATTTGTCCTCCGTTTGGGGATTCGTGAATGAGAGAGTTGCAATTAATAC 1926
Qy      1948 TTATTTTCCACAAATATTTTGGAAAGCACTTCAATAGATTTCACTTTGAAAAAGTA 2007
Db      1927 TTATTTTCCACAAATATTTTGGAAAGCACTTCAATAGATTTCACTTTGAAAAAGTA 1986
Qy      2008 GAGCTGTGTCATAAATCAATATGAGAAAGCTGCTTGCAATCTGAACTTGAGTTTCC 2067
Db      1987 GAGCTGTGTCATAAATCAATATGAGAAAGCTGCTTGCAATCTGAACTTGAGTTTCC 2046
Qy      2068 CTGCAATGAGAAATTTGAATTCGCTCTTTTGAAGAAAAATGATTCACATACAAA 2122
Db      2047 CTGCAATGAGAAATTTGAATTCGCTCTTTTGAAGAAAAATGATTCACATACCAA 2101

RESULT 6
AAF87822
ID   AAF87822 standard; cDNA, 1910 BP.
XX
AC   AAF87822;
XX
DE   11-JUL-2001 (first entry)
XX
DB   Human haemopoietin receptor protein NR12.5 encoding cDNA SEQ ID NO:9.
XX
KW   Human; haemopoietin receptor protein; NR12; immunosuppressive;
XX   anti-allergic; haemopoietin factor; autoimmune disease; tissue rejection;
XX   metal allergy; pollen allergy; ss.
XX
OS   Homo sapiens.
XX
FH   Key Location/Qualifiers
FT   CDS 1..1890
FT   FT  /tag= a
FT   FT  /product= "NR12.5"
FT   FT  /note= "haemopoietin receptor protein"
XX
PN   WO200123556-A1.
XX
PD   05-APR-2001.
XX
PF   27-SEP-2000; 2000MO-JP006654.
XX
PR   27-SEP-1999; 99JP-00273358.
XX   03-AUG-2000; 2000JP-00240397.
XX
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Maeda M, Yaguchi N;
XX
DR   MPI; 2001-26154/27.
XX
DR   P-PDB; AAB74967.
XX
PT   New hemopoietin receptor protein NR12 useful for screening for new
XX   binding factors for potential treatment of autoimmune disease, tissue
XX   rejection and allergies.
XX
PS   Claim 1; Fig 13; 140pp; Japanese.
XX
CC   The present sequence encodes a human haemopoietin receptor protein NR12
XX   designated NR12.5. NR12 has immunosuppressive and anti-allergic

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CC activities. NR12 can be used for searching for haemopoietin factors with
CC the potential for controlling autoimmune disease, Tissue rejection and
CC allergies against e.g. metals and pollen
XX

Sequence 1910 BP; 654 A; 379 C; 352 G; 525 T; 0 U; 0 Other;

Query Match 66.7%; Score 1906; DB 5; Length 1910;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1906; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
QY 119 ATGATATCAGTCACTATTCATGAGATGCAATATAGCCCTTACATCTCTTCACTGG 178
DB 1 ATGATATCAGTCACTATTCATGAGATGCAATATAGCCCTTACATCTCTTCACTGG 60
QY 179 TGTCAATGAGGATTTCAATATATATCTGCTGCGCCACATCTGGGAGAACAGCCACA 238
DB 61 TGTCAATGAGGATTTCAATATATATATCTGCTGCGCCACATCTGGGAGAACAGCCACA 120
QY 239 ATTTTAAATGAGGATTTCAATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 298
DB 121 ATTTTAAATGAGGATTTCAATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 180
QY 299 CCAAGGAACTCTATTTTATATATATGCGATCAAGAAAGATTTCAATCACAAGATT 358
DB 181 CCAAGGAACTCTATTTTATATATATGCGATCAAGAAAGATTTCAATCACAAGATT 240
QY 359 AATATATCAACAGCTGGCTTTGATATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 418
DB 241 AATATATCAACAGCTGGCTTTGATATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 300
QY 419 TGTCAATGAGGATTTCAATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 478
DB 301 TGTCAATGAGGATTTCAATATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 360
QY 479 TGTGATATCTGCGCAGATATCTGATATGATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 538
DB 361 TGTGATATCTGCGCAGATATCTGATATGATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 420
QY 539 AACATATCTGCGCAGATATCTGATATGATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 598
DB 421 AACATATCTGCGCAGATATCTGATATGATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 480
QY 599 CATGTAAGAGGATTTGATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 658
DB 481 CATGTAAGAGGATTTGATATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 540
QY 659 ATCTCAGTATTCATTAACAAGGTGCAAGATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 718
DB 541 ATCTCAGTATTCATTAACAAGGTGCAAGATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 600
QY 719 GCACTGAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 778
DB 601 GCACTGAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 660
QY 779 TGTGAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 838
DB 661 TGTGAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 720
QY 839 TATGAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 898
DB 721 TATGAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 780
QY 899 ACAATCAACAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 958
DB 781 ACAATCAACAGGATTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 840
QY 959 GAATTTCTAGTGAAGCAATTAAGATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 1018
DB 841 GAATTTCTAGTGAAGCAATTAAGATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 900
QY 1019 AAAAGGATCTGAGGCTTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 1078
DB 901 AAAAGGATCTGAGGCTTTGATATATCTGCTGCGCCACAGCAATTAAGAACTGCCAA 960
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QY 1079 CAGGTACATCAAAAGCATTTCCAAATGACACATGAAATTTGGGCTTACAGTTGCTTCC 1138
DB 961 CAGGTACATCAAAAGCATTTCCAAATGACACATGAAATTTGGGCTTACAGTTGCTTCC 1020
QY 1139 ATCTTCAAGGAGCATTTCTGACCAACAGAGAGACATTTGATTTTGGGATG 1198
DB 1021 ATCTTCAAGGAGCATTTCTGACCAACAGAGAGACATTTGATTTTGGGATG 1080
QY 1199 ATGCTCTTGGCTGATATGTTGATATCTTCTTGGATTTTGAATCAATCTTC 1258
DB 1081 ATGCTCTTGGCTGATATGTTGATATCTTCTTGGATTTTGAATCAATCTTC 1140
QY 1259 CGAAGTGGATTTAAAGAGGATCTTATGTTTAAATCAAGAGGCTTTTGAAGATTT 1318
DB 1141 CGAAGTGGATTTAAAGAGGATCTTATGTTTAAATCAAGAGGCTTTTGAAGATTT 1200
QY 1319 CCTATATGAAAAACAGCAATGTTGTAAATGCTTACAGGAAAAATGTAATCTTATGAAAT 1378
DB 1201 CCTATATGAAAAACAGCAATGTTGTAAATGCTTACAGGAAAAATGTAATCTTATGAAAT 1260
QY 1379 AATATTTCAAGTGAAGAGTCTTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1438
DB 1261 AATATTTCAAGTGAAGAGTCTTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1320
QY 1439 TTCAATCCCAAGACAGAGGCTTACAGCTTACAGAGAGAGATACAGGACCCCTGAGACA 1498
DB 1321 TTCAATCCCAAGACAGAGGCTTACAGCTTACAGAGAGAGATACAGGACCCCTGAGACA 1380
QY 1499 AGAGACTACCCGCAAAATCTGCTATTCGACAAATCTACAGTGTATATATCTGATCTC 1558
DB 1381 AGAGACTACCCGCAAAATCTGCTATTCGACAAATCTACAGTGTATATATCTGATCTC 1440
QY 1559 AACATGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCTGAGCAAT 1618
DB 1441 AACATGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCTGAGCAAT 1500
QY 1619 AATATGAAATTAATCTTCTTAAACACTTAAACCAAGAGTGTCTTAACTGAGCAAT 1678
DB 1501 AATATGAAATTAATCTTCTTAAACACTTAAACCAAGAGTGTCTTAACTGAGCAAT 1560
QY 1679 AATCCAGGTTACAAAGCATCTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1738
DB 1561 AATCCAGGTTACAAAGCATCTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1620
QY 1739 AGCAACAAATTTTCTTGAAGATTAAGCTCTATTTAAATCAAGAGATGCACTTCT 1798
DB 1621 AGCAACAAATTTTCTTGAAGATTAAGCTCTATTTAAATCAAGAGATGCACTTCT 1680
QY 1799 CCTGACATCAAAACCTGATGAGAGGAGAACCAAGCTTTTGAAGAAATGATCAACC 1858
DB 1681 CCTGACATCAAAACCTGATGAGAGGAGAACCAAGCTTTTGAAGAAATGATCAACC 1740
QY 1859 AGTGAATGAGAGTGGCATCTTAAATCTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1918
DB 1741 AGTGAATGAGAGTGGCATCTTAAATCTTAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1800
QY 1979 TTCAATGAGATTTCTTCTTGAAGAAATGAGCTGTGTGCAAAATCA 2028
DB 1861 TTCAATGAGATTTCTTCTTGAAGAAATGAGCTGTGTGCAAAATCA 1910
```

RESULT 7
ADV43392
ID ADV43392 standard; cDNA; 1890 BP.
AC
XX ADV43392;
XX
DT 10-MAR-2005 (first entry)

Db 1501 AATTAAGAAATTTCTTCTTAACCTTAACACAGTGTATTCCTTAGACTCAGGAAT 1560
 Qy 1679 AATCCCAAGTTACAAAAGCATCTTAATTTGCTTTCTGTTCAAGTGAATTCCTA 1738
 Db 1561 AATCCCAAGTTACAAAAGCATCTTAATTTGCTTTCTGTTCAAGTGAATTCCTA 1620
 Qy 1739 AGCAACCAATATTTCTTGGAGATTAAGCCTCATATTAATCAAGAGATGCAATTCT 1798
 Db 1621 AGCAACCAATATTTCTTGGAGATTAAGCCTCATATTAATCAAGAGATGCAATTCT 1680
 Qy 1799 CCTGACATACAAAACCTCAGTAGAGAGAAACCAACATGCTTTGGAAAATGATCACCC 1858
 Db 1681 CCGACATACAAAACCTCAGTAGAGAGAAACCAACATGCTTTGGAAAATGATCACCC 1740
 Qy 1859 AGTGAACCTATTTCCAGAACGACCCCTGCTTCCGATGAATTTGCTCTGTTGGGATC 1918
 Db 1741 AGTGAACCTATTTCCAGAACGACCCCTGCTTCCGATGAATTTGCTCTGTTGGGATC 1800
 Qy 1919 GTGAATGAGAGTTCATCATATTAATTAATTTTCCAAAATATTTTGGAAAGCCAC 1978
 Db 1801 GTGAATGAGAGTTCATCATATTAATTAATTTTCCAAAATATTTTGGAAAGCCAC 1860
 Qy 1979 TTCAATAGATTTCACTCTTGGAAAAGTAG 2008
 Db 1861 TTCAATAGATTTCACTCTTGGAAAAGTAG 1890

RESULT 8
 AAD38774
 ID AAD38774 standard; DNA; 1698 BP.
 XX AAD38774;

DT 23-SBP-2002 (first entry)
 DE Human haematopoietin receptor 2 (HPR2) ex8-ex9 DNA.

XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
 KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 KW neurodegenerative disorder; carcinoma; haematologic disorder;
 KW cancer; myeloid myeloid aplastic disorder; idiopathic thrombocytopenic purpura;
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KW osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KW ischemic disease; gene; ds.

XX Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 1..1698
 FT /*tag= a
 TT /product= "Human HPR2 ex8-ex9 protein"

PN WO200229060-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001MO-US031634.

PR 06-OCT-2000; 2000US-0238706P.

PR 13-OCT-2000; 2000US-0240476P.

PR 20-FEB-2001; 2001US-0270282P.

PA (IMMV) IMMUNEX CORP.

PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;

DR WPI; 2002-330172/36.
P-PSDB; AAE24034.

XX Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions.

Claim 9, Page 123-124, 136pp; English.

The present invention relates to human and murine haematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various hematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocy-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as
 CC osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polynuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, stroke including
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence is
 CC human HPR2 ex8-ex9 DNA

SQ Sequence 1698 BP; 597 A; 335 C; 310 G; 456 T; 0 U; 0 Other;

Query Match 52.3%; Score 1493.6; DB 6; Length 1698;
 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 1695; Conservative 2; Mismatches 1; Indels 192; Gaps 1;

Qy 119 ATGAATCAKCTCACTATTCAGTGGATGCAATTAAGCCCTTACATCTCTTCAAGCTGG 178
 Db 1 ATGAATCAGGTCACTATTCAGTGGATGCAATTAAGCCCTTACATCTCTTCAAGCTGG 60
 Qy 179 TGTGATGAGAGATTTACAAATATTAATCTGCTGGCCACATCTGGTGAAGAACGACCA 238
 Db 61 TGTGATGAGAGATTTACAAATATTAATCTGCTGGCCACATCTGGTGAAGAACGACCA 120
 Qy 239 ATTTTAAGATGGGTATGAATATCTCTATATATTTGCCAAGCAGCAATTAAGACTGCCAA 298
 Db 121 ATTTTAAGATGGGTATGAATATCTCTATATATTTGCCAAGCAGCAATTAAGACTGCCAA 180
 Qy 299 CCAAGGAACTTCATTTTATATAAATGCGATCAAGAAAGAAATTTCAATCAAGAGATT 358
 Db 181 CCAAGGAACTTCATTTTATATAAATGCGATCAAGAAAGAAATTTCAATCAAGAGATT 240
 Qy 359 AATTAACCAACAGCTGGCTTGTATTAATACTTTCTGGAACGACATGCTTATAGTAC 418
 Db 241 AATTAACCAACAGCTGGCTTGTATTAATACTTTCTGGAACGACATGCTTATAGTAC 300
 Qy 419 TGCATGCTGAATGTCCCAACATTTTCAAGAGACATGATATGTGGAAGAAAGCATTTCT 478
 Db 301 TGCATGCTGAATGTCCCAACATTTTCAAGAGACATGATATGTGGAAGAAAGCATTTCT 360
 Qy 479 TCTGATATCCGCGAAGATATCTGATGAAGATACCTGTCTATTAATATTCAGGC 538
 Db 361 TCTGATATCCGCGAAGATATCTGATGAAGATACCTGTCTATTAATATTCAGGC 420

QY 539 AACATGATCTGCACTGGAAATGCTGGAGAGCTCACTACATAGACACAAATACTGTGTA 598
 DB 421 AACATGATCTGCACTGGAAATGCTGGAGAGCTCACTACATAGACACAAATACTGTGTA 480
 QY 599 CATGTGAAGATTTAGAGACAGAAAGAGCAACAGATATCTACCTCAGACTATATTAC 658
 DB 481 CATGTGAAGATTTAGAGACAGAAAGAGCAACAGATATCTACCTCAGACTATATTAC 540
 QY 659 ATCTCCAGCTGATTCATTACAAAGGTGGCAAGATCTTGTTGGGTCCAAAGAGCAAC 718
 DB 541 ATCTCCAGCTGATTCATTACAAAGGTGGCAAGATCTTGTTGGGTCCAAAGAGCAAC 600
 QY 719 GCACTAGGATGGAAGAGTCAAAACAATGCAAAATTCACCTGATGATATAGTATACCT 778
 DB 601 GCACTAGGATGGAAGAGTCAAAACAATGCAAAATTCACCTGATGATATAGTATACCT 660
 QY 779 TCTGCAAGCCGTCACTTTCCAGGGCTGAGACTATATAATGCTACAGTCCCAAGACATATT 838
 DB 661 TCTGCAAGCCGTCACTTTCCAGGGCTGAGACTATATAATGCTACAGTCCCAAGACATATT 720
 QY 839 TATTGGGATGTCAAACAATTTGAAGAGTTTCTGTGAATAGATACAGAGGCTACA 898
 DB 721 TATTGGGATGTCAAACAATTTGAAGAGTTTCTGTGAATAGATACAGAGGCTACA 780
 QY 899 ACAACCCAACTTGAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTCA 958
 DB 781 ACAACCCAACTTGAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTCA 840
 QY 959 GAATTTCTACTGGAGCCAAACATTAAAGTACGATATTTCAAGTGAGTCAAGAAACAGGC 1018
 DB 841 GAATTTCTACTGGAGCCAAACATTAAAGTACGATATTTCAAGTGAGTCAAGAAACAGGC 900
 QY 1019 AAAAGGACTGGAGCCTTGGAGTTCACGTTTTCATATAACCACTGAAACAGTTCCC 1078
 DB 901 AAAAGGACTGGAGCCTTGGAGTTCACGTTTTCATATAACCACTGAAACAGTTCCC 954
 QY 1079 CAGGTCAATCAAAAGCATTCCAACATGACATGCAATTCGCGGTCAACGTTGCTCC 1138
 DB 955 ----- 954
 QY 1139 ATCTTAAGAGGACCTTACTTCTGACACAGAGAGACATTGGAATTATTTGGGAATG 1198
 DB 955 ----- 954
 QY 1199 ATGCTTTGCTGTATGTTGTCAATCTTCTTTGATGGATATTTAAGATCATTC 1258
 DB 955 ----- 954
 QY 1259 CGAATGGATTTAAAGAGATCTTATGTTAATACCAAGTGGCTTTATGAGATATT 1318
 DB 955 -----GGGATTTAAAGAGATCTTATGTTAATACCAAGTGGCTTTATGAGATATT 1008
 QY 1319 CCTAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGGAAAAATAGTGAATTTATGAAAT 1378
 DB 1009 CCTAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGGAAAAATAGTGAATTTATGAAAT 1068
 QY 1379 AATTAATTCAGTAGAGAGTCTATATGTTGATCCCATGATTCAGAGATATAAGAAATC 1438
 DB 1069 AATTAATTCAGTAGAGAGTCTATATGTTGATCCCATGATTCAGAGATATAAGAAATC 1128
 QY 1439 TTGATCCCAAGACACAGCTTACAGATACAGAGAGAGATACAGAGCCCTGAGACACA 1498
 DB 1129 TTGATCCCAAGACACAGCTTACAGATACAGAGAGAGATACAGAGCCCTGAGACACA 1188
 QY 1499 AGAGACTACCCGCAAAATCTGCTATTCGACAAATACAGAGTTATATTTCTGATCTC 1558
 DB 1189 AGAGACTACCCGCAAAATCTGCTATTCGACAAATACAGAGTTATATTTCTGATCTC 1248
 QY 1559 AAGACTGATATATAACCCCAAAATTTTCAATTTCTGCTGAGGGAACCACTCAGCAAT 1618
 DB 1249 AAGACTGATATATAACCCCAAAATTTTCAATTTCTGCTGAGGGAACCACTCAGCAAT 1308

QY 1619 AATTAAGAAATTAATCTTCTTAACATTAACCAACAGTGTGATCTTTAGACTAGAAAT 1678
 DB 1309 AATTAAGAAATTAATCTTCTTAACATTAACCAACAGTGTGATCTTTAGACTAGAAAT 1368
 QY 1679 AATCCAGGTTACAAAGATCTTAATTTTGCTTTTCTGTTCAAGTGAATTCACATA 1738
 DB 1369 AATCCAGGTTACAAAGATCTTAATTTTGCTTTTCTGTTCAAGTGAATTCACATA 1428
 QY 1739 AGCAACAAATATTTCTTGAGAGATTAAGCTCATATTAATCAAGAGATAGCAATTC 1798
 DB 1429 AGCAACAAATATTTCTTGAGAGATTAAGCTCATATTAATCAAGAGATAGCAATTC 1488
 QY 1799 CCTGACATACAAACTCTAGTAGAGAGAAACCAATGCTTTTGGAAAAATGATTCACCC 1858
 DB 1489 CCTGACATACAAACTCTAGTAGAGAGAAACCAATGCTTTTGGAAAAATGATTCACCC 1548
 QY 1859 AGTGAATCTATTCGAACAGACCCGCTTCCGATGAATTTGTCTGTTTGGGGATC 1918
 DB 1549 AGTGAATCTATTCGAACAGACCCGCTTCCGATGAATTTGTCTGTTTGGGGATC 1608
 QY 1919 GTGAATGAGAGTGGCATCTATTAATCTTATTTTCCAAATAATTTTGGAAAGCCAC 1978
 DB 1609 GTGAATGAGAGTGGCATCTATTAATCTTATTTTCCAAATAATTTTGGAAAGCCAC 1668
 QY 1979 TTCAATAGATTTCACTTTGAAAAATAG 2008
 DB 1669 TTCAATAGATTTCACTTTGAAAAATAG 1698

RESULT 9
 AAK98258
 ID AAK98258 standard; DNA; 1887 BP.
 XX
 AC AAK98258;
 DT 28-MAY-2002 (first entry)
 XX
 DE Human DNAX cytokine receptor subunit 5 (DCR85) reverse translation DNA.
 XX
 KW Human: DNAX cytokine receptor subunit 5; DCR85; IL30 receptor;
 KW immune response; DCR5; p40/IL-30 ligand; cell physiology modulation;
 KW cell development modulation; TH1-mediated disease; multiple sclerosis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW diabetes; psoriasis; sepsis; allogeneic transplant; recipient;
 KW TH2 response; tumour; viral growth; fungal growth; vaccine;
 KW allergic response; ss; reverse translation.
 XX
 OS Homo sapiens.
 XX
 PN NC0200185790-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 10-MAY-2001; 2001MO-US015057.
 XX
 PR 10-MAY-2000; 2000US-0203426P.
 XX
 PA (SCHB) SCHERING CORP.
 XX
 PI Chirica M, Kastelein RA, Moore KW, Parham CL;
 XX
 DR WPI; 2002-062238/08.
 XX
 PT Novel DNAX cytokine receptor subunit 5 polypeptide which is subunit of
 PT receptor complex for p40/IL-30, useful for treating conditions
 PT associated with abnormal expression or triggering of response to p40/IL-
 PT B30 ligand.
 XX
 PS Disclosure; Page 13; 74pp; English.
 CC The present DNA sequence represents a reverse translation of the human
 CC DNAX cytokine receptor subunit 5 (defined as DCR85 or IL30 receptor) of
 CC the invention. DCR85 is a member of the class I branch of the cytokine

Db 1267 GTTAATACCAAGGCTTTATGAGATATCTTAATATGAAAAACGCAATGTTGAA 1326
QY 1348 AATGCTACAG 1357
Db 1327 AATGCTACAG 1336

RESULT 11
AA87821
ID AA87821 standard; cDNA; 1301 BP.
XX AAF87821;
XX
XX 11-JUL-2001 (first entry)
XX
XX Human haemopoietin receptor protein NR12.4 encoding cDNA SEQ ID NO:7.
XX
XX Human haemopoietin receptor protein; NR12; immunosuppressive;
XX anti-allergic; haemopoietin factor; autoimmune disease; tissue rejection;
XX metal allergy; pollen allergy; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1287
XX FT /*tag= a
XX FT /product= "NR12.4"
XX FT /note= "haemopoietin receptor protein"
XX
XX PN W0200123556-A1.
XX PD 05-APR-2001.
XX 27-SEP-2000; 2000WO-JP006654.
XX PF 27-SEP-1999; 99JP-00273358.
XX PR 03-AUG-2000; 2000JP-00240397.
XX
XX (CHUG) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX Maeda M, Yaguchi N;
XX
XX WPI; 2001-266154/27.
XX DR P-PDB; AAB74966.
XX
XX New haemopoietin receptor protein NR12 useful for screening for new
XX PT binding factors for potential treatment of autoimmune disease, tissue
XX PT rejection and allergies.
XX
XX Claim 1; Fig 11; 140pp; Japanese.
XX
XX The present sequence encodes a human haemopoietin receptor protein NR12
XX designated NR12.4. NR12 has immunosuppressive and anti-allergic
XX activities. NR12 can be used for searching for haemopoietin factors with
XX the potential for controlling autoimmune disease, tissue rejection and
XX allergies against e.g. metals and pollen
XX
XX Sequence 1301 BP; 432 A; 253 C; 262 G; 354 T; 0 U; 0 Other;
XX

Query Match 43.3%; Score 1236.6; DB 5; Length 1301;
Best local Similarity 99.8%; Pred. No. 7.5e-297;
Matches 1236; Conservaive 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 ATGAATCACTCACTATTCATGAGATGAGTAATAGCCCTTTACATACCTCTTCACTGG 178
Db 1 ATGAATCACTCACTATTCATGAGATGAGTAATAGCCCTTTACATACCTCTTCACTGG 60
QY 179 TGTCACTGAGATTTAATAATATTAATGCTCTGGCCCAATCTGGGTAGAACGACGACA 238
Db 61 TGTCACTGAGATTTAATAATATTAATGCTCTGGCCCAATCTGGGTAGAACGACGACA 120
QY 239 ATTTTAAGATGGGTATGATATCTCTATATATTGCCAAGCAGCAATTAAGAACTGCCAA 298

Db 121 ATTTTAAGATGGGTATGATATCTCTATATATTGCCAAGCAGCAATTAAGAACTGCCAA 180
QY 299 CCAAGAACTTCACTTTTATTAATAATGCAATCAAGAAAGATTTCATAATCACAAGATT 358
Db 181 CCAAGAACTTCACTTTTATTAATAATGCAATCAAGAAAGATTTCATAATCACAAGATT 240
QY 359 AATTAACAACACAGCTGCTTGTGTATTAATACTTCTGAGACACATGCTTCTATGTAC 418
Db 241 AATTAACAACACAGCTGCTTGTGTATTAATACTTCTGAGACACATGCTTCTATGTAC 300
QY 419 TGCATGCTGAATGTCCCAAACTTTTCAAGAGACATGATATGTGAAAAAGCATTTCT 478
Db 301 TGCATGCTGAATGTCCCAAACTTTTCAAGAGACATGATATGTGAAAAAGCATTTCT 360
QY 479 TCTGATATCCGCGAATATTCCTGATGATGATACCTGTCTATTATGAAATTCAGGC 538
Db 361 TCTGATATCCGCGAATATTCCTGATGATGATACCTGTCTATTATGAAATTCAGGC 420
QY 539 AACATGACTTGCACCTGGAATGCTTGGAGCTCACCTACATAGACAAATAATCGTGTG 598
Db 421 AACATGACTTGCACCTGGAATGCTTGGAGCTCACCTACATAGACAAATAATCGTGTG 480
QY 599 CATGTGAAGATTGAAGACAGAAAGAGCAACAGTATCTCACTCACTATATTAAAC 658
Db 481 CATGTGAAGATTGAAGACAGAAAGAGCAACAGTATCTCACTCACTATATTAAAC 540
QY 659 ATCTCCAGATTCATTAACAAGGTGCGCAAGAACTACTGTGTTGGTCCCAAGACAAAC 718
Db 541 ATCTCCAGATTCATTAACAAGGTGCGCAAGAACTACTGTGTTGGTCCCAAGACAAAC 600
QY 719 GCACTAGGATGGAAGATCAAAACAACCTGCAATTCACCTGATGATATAGTACTCT 778
Db 601 GCACTAGGATGGAAGATCAAAACAACCTGCAATTCACCTGATGATATAGTACTCT 660
QY 779 TCTGACCCGCTCATTTCCAGGGCTGAGACTATAATGCTACAGTCCCAAGACATTAAT 838
Db 661 TCTGACCCGCTCATTTCCAGGGCTGAGACTATAATGCTACAGTCCCAAGACATTAAT 720
QY 839 TATTGGATATGTAACAACAATTTGAAAAGTTTCCCTGTGAAATGATCAAGGCTACA 898
Db 721 TATTGGATATGTAACAACAATTTGAAAAGTTTCCCTGTGAAATGATCAAGGCTACA 780
QY 899 ACAACCAAACTTGGATGTTAAGAATTTGACCACTATTTACATATGTCACACAGTCA 958
Db 781 ACAACCAAACTTGGATGTTAAGAATTTGACCACTATTTACATATGTCACACAGTCA 840
QY 959 GAATTCATCTTGGAGCCAAACATTTAAGTATGTTTCAAGTGAATGTCAAGAAACAGGC 1018
Db 841 GAATTCATCTTGGAGCCAAACATTTAAGTATGTTTCAAGTGAATGTCAAGAAACAGGC 900
QY 1019 AAAAGTACTGCGAGCCTTGGAGTTCAACCTTTTTCATTAACAACCTGAAACAGTTCCC 1078
Db 901 AAAAGTACTGCGAGCCTTGGAGTTCAACCTTTTTCATTAACAACCTGAAACAGTTCCC 960
QY 1079 CAGGTACATCAAAAGATTTCAACATGACATGAGATTTCTGGGCTTACAGTTGCTTCC 1138
Db 961 CAGGTACATCAAAAGATTTCAACATGACATGAGATTTCTGGGCTTACAGTTGCTTCC 1020
QY 1139 ATCTTACAGGGACCTTACTTCTGACAAACAGAGAGACATTTGATTTATTTGGGATG 1198
Db 1021 ATCTTACAGGGACCTTACTTCTGACAAACAGAGAGACATTTGATTTATTTGGGATG 1080
QY 1199 ATGCTCTTGGCTGTATGTGTGCAATTTCTTTTGAATGGGATTTTACATCATTTTC 1258
Db 1081 ATGCTCTTGGCTGTATGTGTGCAATTTCTTTTGAATGGGATTTTACATCATTTTC 1140
QY 1259 CGAATCGGATTTAAAGAGATCTTATGTTATACCAAGTGGCTTTATGAAATATT 1318
Db 1141 CGAATCGGATTTAAAGAGATCTTATGTTATACCAAGTGGCTTTATGAAATATT 1200
QY 1319 CTTAATATGAAAAACAGCAATGTTTGAATAATCTTACAG 1357

Db	1201	CCTAATATGAAAAAAGACGAATGTTGTGAAAAATGCTACAG	1239
		RESULT 12	
xx		AAC88149	
xx		AAC88149 standard; cDNA; 1155 BP.	
xx			
xx		AAC88149;	
xx			
xx		13-MAR-2001 (first entry)	
xx			
xx		Human DNAX cytokine receptor subunit-2 encoding cDNA SEQ ID NO:1.	
xx			
xx		Human; DNAX cytokine receptor subunit; DCRS2; receptor protein;	
xx		modulating cell proliferation; diagnosis; detection; drug screening;	
xx		immunological disorder; ss.	
xx		Homo sapiens.	
xx		WO200073451-A1.	
xx			
xx		07-DEC-2000.	
xx			
xx		30-MAY-2000; 2000MO-US014867.	
xx			
xx		01-JUN-1999; 99US-00322913.	
xx			
xx		(SCHE) SCHERING CORP.	
xx			
xx		Dowling LM, Timans JC, Gorman DM, Kastelen RA, Bazan FJ;	
xx		WPI; 2001-061536/07.	
xx		P-PSDB; AAB36646.	
xx			
xx		Novel composition comprising DNAX cytokine receptor subunit polypeptide	
xx		useful for regulating immune system function and for treating	
xx		immunological disorders.	
xx			
xx		Claim 16; Page 10-11; 93pp; English.	
xx			
xx		The present invention describes a composition (I) comprising a	
xx		recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The	
xx		DCRS2 polypeptide is useful for binding ligands and for preparing	
xx		antibodies. The DCRS2 polypeptide is also useful for modulating cell	
xx		proliferation, for diagnostic and therapeutic applications, for detecting	
xx		presence of their ligands and in drug screening assays. It is also useful	
xx		for treating conditions such as immunological disorders. The present	
xx		sequence encodes the human DCRS2 protein	
xx			
xx		Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;	
xx			
xx		Query Match 39.9%; Score 1140.6; DB 4; Length 1155;	
xx		Best Local Similarity 99.7%; Pred. No. 5.3e-273;	
xx		Matches 1151; Conservative 2; Mismatches 1; Indels 1; Gaps 1	
xx			
xx		119 ATGAATCAAGTCATCTATTCATATGCGATGCAATATGAGCCCTTACATCTCTCAGCTGG 178	
xx		1 ATGAATCAGTCATCTATTCATATGCGATGCAATATGAGCCCTTACATCTCTCAGCTGG 60	
xx			
xx		179 TGTCAATGAGGAATTAACAATTAACCTGCTTGGCCACATCTGGGTAGAACCAACGACACA 238	
xx		61 TGTCAATGAGGAATTAACAATTAACCTGCTTGGCCACATCTGGGTAGAACCAACGACACA 120	
xx			
xx		239 ATTTTAAAGATGGGATGAATATCTCTATATATATGCAAGCAGCAATTAAGAACTGCCAA 298	
xx		121 ATTTTAAAGATGGGATGAATATCTCTATATATATGCAAGCAGCAATTAAGAACTGCCAA 180	
xx			
xx		299 CCAAGGAATCTCATTTTATTAATAATGGCATCAAGAAAGATTTCAATCAACAAGATT 358	
xx		181 CCAAGGAATCTCATTTTATTAATAATGGCATCAAGAAAGATTTCAATCAACAAGATT 240	
xx			
xx		359 AATAAACAACAGCTGGCTTGTGTATTAACCTTTCTGAAACCAATGCTTATGTAC 418	

Db	241	AATAAACAACAGCTGGCTTTGGTATATAAAACCTTTCTGAAACCAACATGCTTCATGTAC	300
Oy	419	TGCATCTGTGAATGTCCCAACAATTTTCAAGAGACATGTATATGTGAAAAAGACATTTCT	478
Db	301	TGCATCTGTGAATGTCCCAACAATTTTCAAGAGACATGTATATGTGAAAAAGACATTTCT	360
Oy	479	TCTGGAATATCCGACAGATATTTCTGTAGAGTAACTGTGTCAATTTATGAATATTCAAGC	538
Db	361	TCTGGAATATCCGACAGATATTTCTGTAGAGTAACTGTGTCAATTTATGAATATTCAAGC	420
Oy	539	AACATGACTTGCACCTTGGAAATGCTTGGAACTCACTTACATAGACACAAAATACGTGGTA	598
Db	421	AACATGACTTGCACCTTGGAAATGCTTGGAACTCACTTACATAGACACAAAATACGTGGTA	480
Oy	599	CATGTGAAGATTTTAGAGACAGAAAGAAAGACCAACATCTTCACTCAACTATATTAAAC	658
Db	481	CATGTGAAGATTTTAGAGACAGAAAGAAAGACCAACATCTTCACTCAACTATATTAAAC	540
Oy	659	ATCTCCACTGATTCATTAACAAGGTGGCAAGAAGTACTGGTTTGGGTCCAAAGACCAAC	718
Db	541	ATCTCCACTGATTCATTAACAAGGTGGCAAGAAGTACTGGTTTGGGTCCAAAGACCAAC	600
Oy	719	GCACCTAGAGCATGGAAGAGTCAAAAACAATGCAAAATTCACCTGTAGTAATATGTATCT	778
Db	601	GCACCTAGAGCATGGAAGAGTCAAAAACAATGCAAAATTCACCTGTAGTAATATGTATCT	660
Oy	779	TCTGCAGCCGTCAATTTCCAGGGCTGAGACTATTAATGTCAACAGTGCCTCAAGACATTAAT	838
Db	661	TCTGCAGCCGTCAATTTCCAGGGCTGAGACTATTAATGTCAACAGTGCCTCAAGACATTAAT	720
Oy	839	TATTGGGATATGTCAACAACAATTGAAAAGGTTTCCGTGAAATGAGATCAAGAGCTACA	898
Db	721	TATTGGGATATGTCAACAACAATTGAAAAGGTTTCCGTGAAATGAGATCAAGAGCTACA	780
Oy	899	ACAACCAAACTTGTGAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTCA	958
Db	781	ACAACCAAACTTGTGAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACAGTCA	840
Oy	959	GAATTTCACTTGTGAGCCAAACATTAAGTACGTAATTTCAAGTAGAGTCAAGAAACAGGC	1018
Db	841	GAATTTCACTTGTGAGCCAAACATTAAGTACGTAATTTCAAGTAGAGTCAAGAAACAGGC	900
Oy	1019	AAAAGATACGTGGACCTTGTGAAGTCAACGTTTTTTCATATAACAACCTGAAACAGTTCCC	1078
Db	901	AAAAGATACGTGGACCTTGTGAAGTCAACGTTTTTTCATATAACAACCTGAAACAGTTCCC	960
Oy	1079	CAGGTCAATCAAAAGACATTCACATGACACATGAAATCTGGGCTTAAACAGTTGCTTCC	1138
Db	961	CAGGTCAATCAAAAGACATTCACATGACACATGAAATCTGGGCTTAAACAGTTGCTTCC	1020
Oy	1139	ATCTCTACAGGGACCTTACTTCTGTCAACAAGAGAGACATTTGATTTATTGGGAATG	1198
Db	1021	ATCTCTACAGGGACCTTACTTCTGTCAACAAGAGAGACATTTGATTTATTGGGAATG	1080
Oy	1199	ATGCTCTTTGCTGTATAGTTGTCAATCTTTCTTTGATTTGGGATTTTAAACAATCATTT-	1257
Db	1081	ATGCTCTTTGCTGTATAGTTGTCAATCTTTCTTTGATTTGGGATTTTAAACAATCATTTCC	1140
Oy	1258	CCGAACCTGGGATTAA 1272	
Db	1141	CCGAACCTGGGATTAA 1155	
RESULT 13			
ADCC07176			
ID	ADCC07176 standard; cDNA; 1155 BP.		
XX	ADCC07176;		
XX	AC		
XX	18-DEC-2003 (first entry)		
DT			
DE	DNA encoding human DNAX cytokine receptor subunit 2 (DCR82).		

RESULT 15	
AAD38777	
ID	AAD38777 standard; DNA; 1935 BP.
XX	
AC	
XX	AAD38777;
XX	
DT	23-SEP-2002 (first entry)
XX	
DE	Mouse haematopoietin receptor 2 (HPR2) DNA.
XX	
KW	Mouse; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
KW	pancytopenia; leukopenia; anemia; thrombocytopenia; osteoporosis;
KW	neurodegenerative disorder; leukemia; carcinoma; hematologic disorder;
KW	cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KW	ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
KW	osteoclast disorder; periodontitis; acute polymyopathy; Bell's palsy;
KW	anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
KW	demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
KW	vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KW	stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
KW	ischaemic disease; gene; ds.
XX	
OS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1935
FT	/*tag= a
FT	/product= "Mouse HPR2 protein"
FT	
XX	
PN	WO200229060-A2.
XX	
PD	
XX	11-APR-2002.
XX	
PF	05-OCT-2001; 2001WO-US031634.
XX	
PR	06-OCT-2000; 2000US-0238706P.
PR	13-OCT-2000; 2000US-0240476P.
PR	20-FEB-2001; 2001US-0270282P.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
FI	Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
XX	
DR	WPI; 2002-330172/36.
DR	P-PSDB; AAE24038.
XX	
PT	Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
PT	useful for treating cell proliferation, metabolic, and reproductive
PT	hormone related conditions.
XX	
PS	Claim 9; Page 135-136; 136pp; English.
XX	
XX	The present invention relates to human and murine haematopoietin receptor
CC	polypeptides HPR1 and HPR2. Sequences of the invention are useful for
CC	treating cell proliferation conditions e.g., pancytopenia, leukopenia,
CC	anemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
CC	resulting from a lack of bone-forming cells. They are also useful for
CC	treating cell proliferation conditions such as leukaemia and tumour
CC	metastasis, osteoporosis resulting from an excess of bone-resorbing
CC	cells. HPR sequences are also useful for treating medical conditions and
CC	diseases such as cell proliferation, metabolic and reproductive hormone
CC	related conditions. They are useful for treating various haematologic and
CC	oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
CC	carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
CC	cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
CC	cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
CC	sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
CC	squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
CC	of chronic diseases, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
CC	dysplastic syndromes (including refractory anaemia, refractory anaemia
CC	with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
CC	penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
CC	myeloid metaplasia, osteoclast disorders that lead to bone loss such as

Query Match	38.7%	Score 1105.8	DB 6	Length 1935
Best Local Similarity	75.2%	Pred. No. 2.9e-264		
Matches 1468	Conservative 1	Mismatches 403	Indels 81	Gaps 4
CC	osteoporosis including post-menopausal osteoporosis, periorbitalis			
CC	resulting in tooth loosening or loss, prosthesis loosening after joint			
CC	replacement, neurodegenerative conditions (e.g., acute polymyopathy,			
CC	Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible			
CC	dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,			
CC	Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,			
CC	myasthenia gravis, chronic neuronal degeneration, stroke including			
CC	cerebral ischemic diseases. HPR1 and HPR2 polypeptides are also useful			
CC	for treating various other disorders such as osteoporosis, obesity,			
CC	deficient mammary development and infertility. The present sequence is			
CC	mouse HPR2 DNA			
XX				
SQ	Sequence 1935 BP; 607 A; 420 C; 385 G; 523 T; 0 U; 0 Other;			
Query Match	38.7%	Score 1105.8	DB 6	Length 1935
Best Local Similarity	75.2%	Pred. No. 2.9e-264		
Matches 1468	Conservative 1	Mismatches 403	Indels 81	Gaps 4
QY	119 ATGAATCAKGTCACTTATTCATTTGGATGCAATTAAGCCCTTTACATACTCTTCACTGG	178		
DB	1 ATGAGTCACTCCACACTTCAGCTGATGTGGATAGGCCCTTTATGTGCTCTTCAGATGG	60		
QY	179 TGTCAATGAGGAATTAACAATATTAACGCTCTGGCCCATCTGGGTGGAACGAGCACCA	238		
DB	61 TGTCAAGGAGGAATACAAAGTATTAACGCTCTGGTGAACATGTGGGTGAGCGCTGTGA	120		
QY	239 ATTTTAAAGATGGGATGATATATCTCTATATATTTCCAAAGCAGCAATTAAGAACTGCCAA	298		
DB	121 ATTTTTCAGATGGGATATTAATGTTTCTATATATTTCCAAAGAACCCCTTAAGCATGGCGCA	180		
QY	299 CCAAGAAATCTTCAATTTTATTAATAATGSCATCAAGAAAGATTTCAATCAAGAGATT	358		
DB	181 CCAAGAAATCTTCAATTTTATTAATAATGSCATCAAGAAAGATTTGATATCACAAGAGATT	240		
QY	359 AATAAACAAGAGCTGGCTTGGATATTAATAAATTTTGGAAACCAATGCTCTTATATGATC	418		
DB	241 AATGAACAACAAGAGCTGGATTTGGATTAAGGCTTTTGGAAACCTCATGCTCTTATATGATC	300		
QY	419 TGCACTGCTGATGTCGCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGACATTTCT	478		
DB	301 TGCACTGCTGATGTCGCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGACATTTCT	360		
QY	479 TCTGATATTCGCCAGATATTTCTGATGAAGTAACTGTGTCTTATTAATATATTCAGGC	538		
DB	361 TCTGATATTCGCCAGATATTTCTGATGAAGTAACTGTGTCTTATTAATATATTCAGGC	420		
QY	539 AACATGATTTGCACTCTGGAATGCTTGAAGGCTCACTATATATGACACAAATAATCGTGTA	598		
DB	421 AACATGATTTGCACTCTGGAATGCTTGAAGGCTCACTATATATGACACAAATAATCGTGTA	480		
QY	599 CATGGAAGATTTAGAGACAGAAAGAAAGCAAGTATCTCACTCAAGCTATATATTAAC	658		
DB	481 CATGGAAGATTTAGAGACAGAAAGAAAGCAAGTATCTTGCCTCAAGCTATATTAAG	540		
QY	659 ATCTCACTGATTTCAATTAACAAGTGGCAAGAGTACTTGTTGGTTCACAGCAGCAAAAC	718		
DB	541 ATCTCACTGATTTCAATTAACAAGTGGCAAGAGTATTTGGTTCACAGCAGCAGCAAT	600		
QY	719 GCACTAGGCAATGGAAGTCAAAACATCGCAATTTCACTTGGATGATATAGTATACCT	778		
DB	601 TCCCTAGGCAATGGAAGTCAAAACATCGCAATTTCACTTGGATGATATAGTATACCT	660		
QY	779 TCTGCAAGCGGTCATTTCCAGGGCTGAGCTATTAATGTCTACAGTGGCCAAAGCCATAT	838		
DB	661 TCTGCAAGCGGTCATTTCCAGGGCTGAGCTATTAATGTCTACAGTGGCCAAAGCCATAT	720		
QY	839 TATTGGATAGTCAAAACAACAATTGAAAGGTTTCTTGTGAATAGATATCAAGGCTACA	898		
DB	721 TATTGGATAGTCAAAACAACAATTGAAAGGTTTCTTGTGAATAGATATCAAAACAACA	780		
QY	899 ACAAAACCAACTTGGAAATGTTAAAGATTTTGAACCAATTTTACATATGTGCAAGATCA	958		
DB	781 ACAAAACCAACTTGGAAATGTTAAAGATTTTGAACCAATTTTACATATGTGCAAGATCA	840		

QY 959 GAATTTCTACTGGAGCCAAACATTAAAGTACGTAATTTCAAGTGAATGTCAGAAACAGGC 1018
DB 841 GAATTTCTACTGGAGCCAGACAGCAAGTATGTAATTTCAAGTGAATGTCAGAAACAGGC 900
QY 1019 AAAAGTACTGGAGCCTTGGAGTTCACCGTTTTCATTAACACCTGAA----- 1069
DB 901 AAAAGAACTGGAGCCTTGGAGTTCACCGTTTTCATTAACACCTGAACTGCT 960
QY 1070 -----ACAGTTCC 1078
DB 961 AAAAGAACTGGAGCCTTGGAGTTCACCGTTTTCATTAACACCTGAACTGCT 1020
QY 1079 CAGTCAATCAAAAGCATTCCAAATGACATGACATGAAATTCGGCTTACAGTTGCTTC 1138
DB 1021 CAGGTTACAGCAAAATCATCC---CAGAACTCAGAAATGAGATGTCAGTGTACA 1077
QY 1139 ATCTCTACAGGGACCTTACTTCTGACACAGAGAGACATTTGACTTTTATTTGGGAATG 1198
DB 1078 ATCTCTACAGAGACATCTGCTTCAAGTAAATCAAGACATTTGACTTTTGTGGGAATG 1137
QY 1199 ATCGTCTTGTCTGTATTTGTTCAATTTCTTGTGGAATTTTAAAGATCATTC 1258
DB 1138 GTCTTCTTGGCCATCATGTTGGCAATTTTCTGATTTGGATTTTAAAGATCATTC 1197
QY 1259 CGAATCTGGATTTAAAGAAAGATCTTAATGTTAAATACAAAGTGGCTTTATGAAGATATT 1318
DB 1198 CGAATGGAATTTAAAGAAAGTTTTAACTGATATCCAAAGTGGCTTTATGAAGATATT 1257
QY 1319 CTTAATTTGAAAAAAGCAATGTTTGTGAAAAATGCTACAGAAAAATGTAACCTTATGAAT 1378
DB 1258 CTTAATTTGAAAAAATGCAATGTTGCAAAATTTTACAGAAAAAAGTGTATTGGAAT 1317
QY 1379 AATTAATTCAGTGAAGAGTCTATATGTTGATCCCATGATTAAGAGATAAAAGAAATC 1438
DB 1318 GATTAATTCAGTGAAGAGGCTGTATGATCTGTCTTACAGAGATTAAGTGAATC 1377
QY 1439 TTGATCCAGAACACAAAGCCTTACAGACTACAGAAAGA---GAATAAGAGCCCTGGAG 1495
DB 1378 TCTCCCTGGAACACAAAGCCTTACAGACTTACAAAGAAAGGCTCACAGAGCTCCTGGAG 1437
QY 1496 ACAAGAGACTACCCGCAAACTGCTATTTGACAAATCTACAGTGTATATTTCTGAT 1555
DB 1438 ACAAGAGACTGTCTCTAGGAATGTGTCTACAGATTCCTGTGTGTATATTTCTGAC 1497
QY 1556 CTCACACTGATATATAACCCCAATTTTCAATTTTCTGCTGAGGAGCAATCTCAGC 1615
DB 1498 CTCACACTGATATATAACCCCAATTTTCAATTTTCTGCTGAGGAGCAATCTTTCATT 1557
QY 1616 AATTAATTAATAATTACTTCTTAACAATTAAACACAGTTGATTCCTTAGACTCAGA 1675
DB 1558 AACAGAGATGAAGAGACCTTACATCCCTTGAAGACCAAGATGACACTT----- 1607
QY 1676 AATTAATCCAGGTTACAAAGCATCTTAATTTTGTCTTTTCTGTTTCAAGTGAATTC 1735
DB 1608 -----TGCCGATTTGAAACATATCCCACTTCAATTTTCTGTTCAAGTATGCTTTA 1662
QY 1736 CTAAGCAACACAAATTTCTTGGAAATTAAGCCTCATTTAATCAAGAGAAATGCAGT 1795
DB 1663 CTAAGCAACACAAATTTCTTGGAAATTTGATGAATGTGCTGTTTAAATCAAGAGAAATTCAT 1722
QY 1796 TCTCTGACATACAAACCTCAGTAGAGAGAAACCAATGCTTTTGGAAAAATGATTC 1855
DB 1723 TCTCTGACATTAATAAACTCAGACAGAGAGAAACCAATGCTTTTGGAAAAATGATTC 1782
QY 1856 CCAAGTGAATCTATTCCAGAAACAGACCTGCTTCTGATGAATTTGCTGTTTGGGG 1915
DB 1783 CCAAGTGAATCTATTCCAGAGCAGACTGTGTGTGATGAATTTGCTGTTTGGCA 1842
QY 1916 ATGATGAATGAGAGTGCATATTAATTAATTTTCACAAAATATTTTGAAGAGC 1975
DB 1843 ATGATGAATGAGAGTGCATATTAATTTTCACTTTCACAGAAAGTTTGAAGAGC 1902

QY 1976 CACTTCAATGAGATTCTACTTGGAAAAAGTAG 2008
DB 1903 CATTCAATGAGATTCTACTTGGAAAAAGTAG 1935
Search completed: October 14, 2006, 12:53:55
Job time : 1724 secs

121 GAATCAAGTCACTTATCAATGGAGTGCATTAATGACCTTTACATCTTCAGCTG 180
181 TCATGAGGAATTAACAATATTAATGAGTCTGCGACATCTGGGTAGAACAGCAAT 240
181 TCATGAGGAATTAACAATATTAATGAGTCTGCGACATCTGGGTAGAACAGCAAT 240
241 TTTTAAGATGGGTATGATATCTCTATATATGCGCAAGACATTTAAGAACTCCAA 300
241 TTTTAAGATGGGTATGATATCTCTATATATGCGCAAGACATTTAAGAACTCCAA 300
301 AAGGAACTTCATTTTATATATTAATGAGTCAATGAAAGATTCAATCAAGATTAA 360
301 AAGGAACTTCATTTTATATATTAATGAGTCAATGAAAGATTCAATCAAGATTAA 360
361 TAAACCAAGCTGCGCTTGGTATATTAATGAGTCAATGAAAGATTCAATCAAGATTAA 420
361 TAAACCAAGCTGCGCTTGGTATATTAATGAGTCAATGAAAGATTCAATCAAGATTAA 420
421 CACTGCTGAATGTCCTCAATATTTCAAGAGACATGATATGGAATAAGACATTTCTC 480
421 CACTGCTGAATGTCCTCAATATTTCAAGAGACATGATATGGAATAAGACATTTCTC 480
481 TGAATATCCGCGAGATATTCCTGATGAGTAACTGTCATTTATGATATTCAGGCAA 540
481 TGAATATCCGCGAGATATTCCTGATGAGTAACTGTCATTTATGATATTCAGGCAA 540
541 CATGATCTGACCTGGAATGCTGGAAGCTCACTATATGACCAAAATACGATGATCA 600
541 CATGATCTGACCTGGAATGCTGGAAGCTCACTATATGACCAAAATACGATGATCA 600
601 TGTGAAGATTTAGAGACAGAGAGAGACAAAGTATCTCACTCAAGTATATTAATCAT 660
601 TGTGAAGATTTAGAGACAGAGAGAGACAAAGTATCTCACTCAAGTATATTAATCAT 660
661 CTCGACTGATTCATTAACAGGTGCGAAGAGTACTTGGTGGTCCAGAGCAAGCGC 720
661 CTCGACTGATTCATTAACAGGTGCGAAGAGTACTTGGTGGTCCAGAGCAAGCGC 720
721 ACTAGGATGGAAGAGTCAAAACAACTGCAATTCACCTGATATGATATGATACCTTC 780
721 ACTAGGATGGAAGAGTCAAAACAACTGCAATTCACCTGATATGATATGATACCTTC 780
781 TGCAGCGTATTTCCAGGCTGAGACTATTAATGCTACAGTCCCAAGACATATTTTA 840
781 TGCAGCGTATTTCCAGGCTGAGACTATTAATGCTACAGTCCCAAGACATATTTTA 840
841 TTTGGATATGCAACAAATGGAAGTTTCTGTGAAATGAGATCAAGGCTACAC 900
841 TTTGGATATGCAACAAATGGAAGTTTCTGTGAAATGAGATCAAGGCTACAC 900
901 AAACCAAACTTGAATGTTAAAGATTGACCAATTTTACATATGCAACAGTCA 960
901 AAACCAAACTTGAATGTTAAAGATTGACCAATTTTACATATGCAACAGTCA 960
961 ATTCTACTGAGACCAATTAAGTACATTTCAAGTACATGATGATCAAGGCA 1020
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 2821 GCAACAAAGCAAACTGCTGTCTGAAAAAATTTTAAAAA 2859

RESULT 3
 US-10-720-026-1
 ; Sequence 1, Application US/10720026
 ; Publication No. US2004025868A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chitica, Madeline
 ; APPLICANT: Parham, Christi L.
 ; APPLICANT: Kastelein, Robert A.
 ; APPLICANT: Moore, Kevin W.
 ; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
 ; FILE REFERENCE: DX01074B1K
 ; CURRENT APPLICATION NUMBER: US/10/720, 026
 ; CURRENT FILING DATE: 2003-11-21
 ; PRIOR APPLICATION NUMBER: 60/203, 426
 ; PRIOR FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 2859
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (119)..(2005)
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: (188)..(2005)
 US-10-720-026-1

Query Match 100.0%; Score 2857.4; DB 9; Length 2859;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-667-289-1
; Sequence 1, Application US/10667289
; Publication No. US20050100917A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madeline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelejn, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/10/667,289
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/853,180
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.2
; SEQ ID NO 1
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119) .. (2005)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127) .. (127)
; OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application 48
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (188) .. (2005)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (563) .. (563)
; OTHER INFORMATION: r means g or a. See page 12, line 36, of patent application as
; OTHER INFORMATION: originally filed.
US-10-667-289-1

Query Match 100.0%; Score 2857.4; DB 10; Length 2859;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
 US-10-667-290-1
 ; Sequence 1, Application US/10667290
 ; Publication No. US20050100918A1

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GENERAL INFORMATION:
APPLICANT: Chirica, Madeline
APPLICANT: Parham, Christi L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: DX01074
CURRENT APPLICATION NUMBER: US/10/667,290
CURRENT FILING DATE: 2003-09-18
PRIORITY APPLICATION NUMBER: US/09/853,180B
PRIORITY FILING DATE: 2001-05-10
PRIORITY APPLICATION NUMBER: 60/203,426
PRIORITY FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 2859
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (119)..(2005)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (127)..(127)
OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application as
OTHER INFORMATION: originally filed.
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (188)..(2005)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (563)..(563)
OTHER INFORMATION: r means g or a. See page 12, line 36, of patent application as
OTHER INFORMATION: originally filed.
US-10-667-290-1

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Query Match 100.0%; Score 2857.4; DB 10; Length 2859;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-972-708-19
; Sequence 19, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2830
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-972-708-19
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Best Local Similarity 99.8%; Pred. No. 0;
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DB 1336 AATGCTACAGAAATATGTAATCTTAATGATTAATTTCCAGTGAAGGCTCATATGT 1395
QY 1408 TGAATCCCATGATTAACAGATTAAGAAATCTTCATCCGAAACACAAGCTACAGCTA 1467
DB 1396 TGAATCCCATGATTAACAGATTAAGAAATCTTCATCCGAAACACAAGCTACAGCTA 1455
QY 1468 CAAGAAAGAAATACAGAGCCCTTGAGACAGAGCTACCCGAAACCTGCTATTGGA 1527
DB 1456 CAAGAAAGAAATACAGAGCCCTTGAGAGAGAGCTACCCGAAACCTGCTATTGGA 1515
QY 1528 CAATACACAGTTGATATATATCTGATCTCAACACTGATATTAACCCCAATTTGAA 1587
DB 1516 CAATACACAGTTGATATATATCTGATCTCAACACTGATATTAACCCCAATTTGAA 1575

QY 1588 TTTTCTGCTGAGGAGAGCCATCTCAGCAATATATGAAATTTACTTCTTAACCTTAA 1647
DB 1576 TTTTCTGCTGAGGAGAGCCATCTCAGCAATATATGAAATTTACTTCTTAACCTTAA 1635
QY 1648 ACCACAGTTGATCTCTTAAGCTCAGGAAATATATCCAGGTTACAAAGCATCTTAATTT 1707
DB 1636 ACCACAGTTGATCTCTTAAGCTCAGGAAATATATCCAGGTTACAAAGCATCTTAATTT 1695
QY 1708 TGTCTTTTCTGTTTCAAGTGTGATTTCACTAAGCAACAAATATTTCTTGAGAAATTAAG 1767
DB 1696 TGTCTTTTCTGTTTCAAGTGTGATTTCACTAAGCAACAAATATTTCTTGAGAAATTAAG 1755
QY 1768 CCTCATATTAATCAAGAGAAATGCACTTCTCTGACATACAAATCTCAGTAGAGAGA 1827
DB 1756 CCTCATATTAATCAAGAGAAATGCACTTCTCTGACATACAAATCTCAGTAGAGAGA 1815
QY 1828 AACACAGCTTTTGGAAAAATGATCACCAGTGAAACATATTCAGAAACAGACCTGTGCT 1887
DB 1816 AACACAGCTTTTGGAAAAATGATCACCAGTGAAACATATTCAGAAACAGACCTGTGCT 1875
QY 1888 TCTGTGATGATTTGTCTCCTGTTTGGAGATCGTGAATGAGAGTTGCCATCTATTAATAC 1947
DB 1876 TCTGTGATGATTTGTCTCCTGTTTGGAGATCGTGAATGAGAGTTGCCATCTATTAATAC 1935
QY 1948 TATATTTTCCAAAAATATTTTGGAAAGCACTTCAATAGATTTCACTTGAAAAAGTA 2007
DB 1936 TATATTTTCCAAAAATATTTTGGAAAGCACTTCAATAGATTTCACTTGAAAAAGTA 1995
QY 2008 GAGCTGTGTGTGCAAAATCAATATGAGAAAGGCTGTCATCTGAACTTGAGGTTTTCC 2067
DB 1996 GAGCTGTGTGTGCAAAATCAATATGAGAAAGGCTGTCATCTGAACTTGAGGTTTTCC 2055
QY 2068 CTGCAATAGAAATTTGAAATCTGCTCTTTTGGAAAAATGTAATTCATACATCAATCTTC 2127
DB 2056 CTGCAATAGAAATTTGAAATCTGCTCTTTTGGAAAAATGTAATTCATACATCAATCTTC 2115
QY 2128 ACATGACACATGTTTCAATTTCTCTTGATTAATACCTAAGTAGAGGATTTCTGGGCA 2187
DB 2116 ACATGACACATGTTTCAATTTCTCTTGATTAATACCTAAGTAGAGGATTTCTGGGCA 2175
QY 2188 TATGATAGCATATGTTTCAATTTCTCTTGATTAATACCTAAGTAGAGGATTTCTGGG 2247
DB 2176 TATGATAGCATATGTTTCAATTTCTCTTGATTAATACCTAAGTAGAGGATTTCTGGG 2235
QY 2248 CTCCTACATCAACAGTAAAGATTTCCGAGAGCTCATGCTTTTAAATTTTAAAGCAT 2307
DB 2236 CTCCTACATCAACAGTAAAGATTTCCGAGAGCTCATGCTTTTAAATTTTAAAGCAT 2295
QY 2308 CTTCTGCTMAATTTCTTAAATTTAGAAATTAAGGTTCCGAAAGTGAACATGCTTCATG 2367
DB 2296 CTTCTGCTMAATTTCTTAAATTTAGAAATTAAGGTTCCGAAAGTGAACATGCTTCATG 2355
QY 2368 GTACACATACAGGCAAAACAGATTAATGAGAGGCTCATGATTTTATTAAGAGT 2427
DB 2356 GTACACATACAGGCAAAACAGATTAATGAGAGGCTCATGATTTTATTAAGAGT 2415
QY 2428 CAATATTTCTCTTATTTTCCCTCATGAAAGATGCAAAACAGCTCTCATATGTGTAC 2487
DB 2416 CAATATTTCTCTTATTTTCCCTCATGAAAGATGCAAAACAGCTCTCATATGTGTAC 2475
QY 2488 AGAAAGGTAATATGCAAAATACCTGATGTAATTAATATGCTGAAAAATTTCTTTA 2547
DB 2476 AGAAAGGTAATATGCAAAATACCTGATGTAATTAATATGCTGAAAAATTTCTTTA 2535
QY 2548 AATTAATCATATAGGCGAGGCGTGTGTGCTCATGCTTAAATCCAGACCTTTGGTAGG 2607
DB 2536 AATTAATCATATAGGCGAGGCGTGTGTGCTCATGCTTAAATCCAGACCTTTGGTAGG 2595
QY 2608 CTGAGGTGTGTGATCACTGAGGTGAGAGTTCAGAGTCCAGGCTGCGCAATATGTGTA 2667
DB 2596 CTGAGGTGTGTGATCACTGAGGTGAGAGTTCAGAGTCCAGGCTGCGCAATATGTGTA 2655
QY 2668 ACCCTGTCTCTAATAAATTAACAAAAATTAAGCCGAGCAATGTGTGCAAGTGTGTAATCC 2727


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Db      1576 TTTCTGCGCTGAGGAGGAGCATCTCAGCAATTAATAAGAAATTAATCTTAACTTAACTTAA 1635
Qy      1648 ACCACGAGTGAATTCCTTAGACCTCAGGAATTAATCCAGGTTCAAAAGATCCTAATTT 1707
Db      1636 ACCACGAGTGAATTCCTTAGACCTCAGGAATTAATCCAGGTTCAAAAGATCCTAATTT 1695
Qy      1708 TGCCTTTCTGTTCAAGTGAATTCATTAAGCAACAATATTTCTTGAGAAATTAAG 1767
Db      1696 TGCCTTTCTGTTCAAGTGAATTCATTAAGCAACAATATTTCTTGAGAAATTAAG 1755
Qy      1768 CTTCAATTTAATTAAGAGATGCAAGTTCTCTGACATACAAATCTCACTAGTAGAGAGA 1827
Db      1756 CTTCAATTTAATTAAGAGATGCAAGTTCTCTGACATACAAATCTCACTAGTAGAGAGA 1815
Qy      1828 AACACCATGCTTTTGAAGAAATGATCAACCAGGAAATCTATTCAGAACAGACCCGCT 1887
Db      1816 AACACCATGCTTTTGAAGAAATGATCAACCAGGAAATCTATTCAGAACAGACCCGCT 1875
Qy      1888 TCCTGATGAATTTGCTCTGTTTGGGGAATCGTAATGAGAGATTGTCATTAATTAAC 1947
Db      1876 TCCTGATGAATTTGCTCTGTTTGGGGAATCGTAATGAGAGATTGTCATTAATTAAC 1935
Qy      1948 TTAATTTTCACAAAATATTTTGAAGCACTTCATAGATTTCACTTTGAGAAAGTA 2007
Db      1936 TTAATTTTCACAAAATATTTTGAAGCACTTCATAGATTTCACTTTGAGAAAGTA 1995
Qy      2008 GAGCTGTGTGTCAAATTAAGAAAGCTGCTTGAACCTGAACTTGAGCTTGGTTTCC 2067
Db      1996 GAGCTGTGTGTCAAATTAAGAAAGCTGCTTGAACCTGAACTTGAGCTTGGTTTCC 2055
Qy      2068 CTGCAATAGAAATGAATTCGCTCTTTTGAAGAAATGATTAATCAATCAATCTTC 2127
Db      2056 CTGCAATAGAAATGAATTCGCTCTTTTGAAGAAATGATTAATCAATCAATCTTC 2115
Qy      2128 ACATGACACATGTTTCAATTTCCCTTGATAAATACCTAGTAGAGGATTTGCTGGCCA 2187
Db      2116 ACATGACACATGTTTCAATTTCCCTTGATAAATACCTAGTAGAGGATTTGCTGGCCA 2175
Qy      2188 TATGATTAAGCAATATGTTGCTTACCAATCTGTTTCCAGATAGTGAATTTCTGAG 2247
Db      2176 TATGATTAAGCAATATGTTGCTTACCAATCTGTTTCCAGATAGTGAATTTCTGAG 2235
Qy      2248 CTCTCAATCAATCAGATGAATTTCCCGGAGCTCAGATGCTTTTAAATTTAGCAAT 2307
Db      2236 CTCTCAATCAATCAGATGAATTTCCCGGAGCTCAGATGCTTTTAAATTTAGCAAT 2295
Qy      2308 CTCTGCTTAAATTTCTTAAATTAAGAAATTAAGGTCGCCAGAGTGAACAATGCTTCATG 2367
Db      2296 CTCTGCTTAAATTTCTTAAATTAAGAAATTAAGGTCGCCAGAGTGAACAATGCTTCATG 2355
Qy      2368 GTCCACATACAGGACCAAAAACAGCATTAATGTCAGAGCTCAGATTTTAAATTAAGT 2427
Db      2356 GTCCACATACAGGACCAAAAACAGCATTAATGTCAGAGCTCAGATTTTAAATTAAGT 2415
Qy      2428 CAATATTTTCTCTTAAATTTCTCTCAATGAAAGATCAAAAGAGCTCTCTAATGTGTAC 2487
Db      2416 CAATATTTTCTCTTAAATTTCTCTCAATGAAAGATCAAAAGAGCTCTCTAATGTGTAC 2475
Qy      2488 AGAAGAGGTAAATTAATGCAAAATTAATGTAATTAATTAATTAATTAATTAATTAAT 2547
Db      2476 AGAAGAGGTAAATTAATGCAAAATTAATGTAATTAATTAATTAATTAATTAATTAAT 2535
Qy      2548 AAAATAGAAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2607
Db      2536 AAAATAGAAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2595
Qy      2608 CTGAGTGTGATGATCACTGAGGAGTCAAGAGTTCAGATGCAAGCTGAGGCAATATGTGAA 2667
Db      2596 CTGAGTGTGATGATCACTGAGGAGTTCAGATGCAAGCTGAGGCAATATGTGAA 2655
Qy      2668 ACCCTGTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2727

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Db      2656 ACCCTGTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2715
Qy      2728 CAGCTACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2787
Db      2716 CAGCTACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2775
Qy      2788 GAGCTGAGATTTGGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCTC 2842
Db      2776 GAGCTGAGATTTGGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCTC 2830

RESULT 8
US-10-105-930-5
; Sequence 5, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Meade, Maestru
; APPLICANT: Yaguchi, No. US20030009018A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U81
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ. ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98) ... (1984)
; US-10-105-930-5

Query Match      72.8%; Score 2081.4; DB 6; Length 2123;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2085; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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427 AGAGACGTATATATGAAAAAGACATTTCTTCTGATATCCGACAGATATTCCTGATGA 486
508 AGTAACTGCTGCTATTTATGAAATATTCAGGCAATGATCTTGACCTGAAATGCTGGAA 567
487 AGTAACTGCTGCTATTTATGAAATATTCAGGCAATGATCTTGACCTGAAATGCTGGAG 546
568 GCTCACTGATAGACACAAATACGTGTACATGTGAAGAGTTAGACAGAAAGAA 627
547 GCTCACTGATAGACACAAATACGTGTACATGTGAAGAGTTAGACAGAAAGAA 606
628 GCAACAGATATCTCACTCAAGCTATTTAAATCACTGATTCATTAAGAGTGC 687
607 GCAACAGATATCTCACTCAAGCTATTTAAATCACTGATTCATTAAGAGTGC 666
688 GAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 747
667 GAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726
748 GCAAAATTCACCTGATATATGATATCTTCTGACGCTGCTGCTGCTGCTGCTGCTGCT 807
727 GCAAAATTCACCTGATATATGATATCTTCTGACGCTGCTGCTGCTGCTGCTGCTGCT 786
808 TATTAATGCTACAGTGTCCCAAGACCAATTTATGCTGATATGCTGATGCTGATGCT 867
787 TATTAATGCTACAGTGTCCCAAGACCAATTTATGCTGATATGCTGATGCTGATGCT 846
868 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 927
847 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
928 TGAACCAATTTTATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 987
907 TGAACCAATTTTATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
988 GCTATTTCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
967 GCTATTTCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1026
1048 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
1027 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
1108 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1167
1087 GCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
1168 GCAAGGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227
1147 GCAAGGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
1228 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1287
1207 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
1288 GTTAAATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1347
1267 GTTAAATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
1348 AATGCTACAGGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1407
1327 AATGCTACAGGAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
1408 TGAATCCATATTAAGAGATATTAAGAGATATTAAGAGATATTAAGAGATATTAAGAGAT 1467
1387 TGAATCCATATTAAGAGATATTAAGAGATATTAAGAGATATTAAGAGATATTAAGAGAT 1446
1468 CAAGAAAGAAATATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1527
1447 CAAGAAAGAAATATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
1528 CAATATCAAGTGTATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1587
1507 CAATATCAAGTGTATATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566

1588 TTTTCTGCTGAGGAGAGCCATCTCAGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1647
1567 TTTTCTGCTGAGGAGAGCCATCTCAGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1626
1648 ACCACAGTGTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1707
1627 ACCACAGTGTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
1708 TGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1767
1687 TGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1746
1768 CTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1827
1747 CTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1806
1828 AACCAACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1887
1807 AACCAACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
1888 TCTGATGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1947
1867 TCTGATGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1926
1948 TTAATTTTCAAAATATTTTGGAAAGCCACTTCAATAGATTTCACTTGGAAAGTA 2007
1927 TTAATTTTCAAAATATTTTGGAAAGCCACTTCAATAGATTTCACTTGGAAAGTA 1986
2008 GAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2067
1987 GAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2046
2068 CTGCAATGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2122
2047 CTGCAATGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2101

RESULT 9
US-10-105-930-9
; Sequence 9, Application US/10105930
; Publication No. US2003009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Maatsugu
; APPLICANT: Yasuuchi, No. US2003009018A1:ko
; TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105, 930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1887)
US-10-105-930-9

Query Match 66.7%; Score 1906; DB 6; Length 1910;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1906; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

119 ATGAATCAGTCACTATTTCAATGAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 178
1 ATGAATCAGTCACTATTTCAATGAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 60

OY	179	TGTCATGAGGAATTAACAATAATATAAAGCTGCTGGCCACATCTGGGTGAACGACGACA	238
Db	61	TGTCATGAGGAATTAACAATAATATAAAGCTGCTGGCCACATCTGGGTGAACGACGACA	120
OY	239	ATTTTAAAGATGGGTATGATATCTCTATATATTTGCCAAGCAGCAATTAAAGACTGCCAA	298
Db	121	ATTTTAAAGATGGGTATGATATCTCTATATATTTGCCAAGCAGCAATTAAAGACTGCCAA	180
OY	299	CCAAAGGAACCTTCATTTTATATATAAATGGCAATCAAGAAAGTTTCAATCAACAAGATT	358
Db	181	CCAAAGGAACCTTCATTTTATATATAAATGGCAATCAAGAAAGTTTCAATCAACAAGATT	240
OY	359	AATAAAACAAGCTCGGCTTTGGTATATAAAACCTTCTGAAACCAATGCTTCTATGTAC	418
Db	241	AATAAAACAAGCTCGGCTTTGGTATATAAAACCTTCTGAAACCAATGCTTCTATGTAC	300
OY	419	TGCACTGTGTAATGTCCCAAACTTTTCAAGACACATGATATGTGAAAAAGACATTTCT	478
Db	301	TGCACTGTGTAATGTCCCAAACTTTTCAAGACACATGATATGTGAAAAAGACATTTCT	360
OY	479	TCTGGATATCCGCAGATATTCCTGATAGATTAACCTGTGTCAATTATGAATATTCAGAC	538
Db	361	TCTGGATATCCGCAGATATTCCTGATAGATTAACCTGTGTCAATTATGAATATTCAGAC	420
OY	539	AACATGACTTGCACCTGGAAATGCTTGGAACTCACCTTACATAGACACAAATACGTGTA	598
Db	421	AACATGACTTGCACCTGGAAATGCTTGGAACTCACCTTACATAGACACAAATACGTGTA	480
OY	599	CATGTAAGAGTTTAGAGACAGAAAGACAGTAATCTCACTCAAGCTATTTATAC	658
Db	481	CATGTAAGAGTTTAGAGACAGAAAGACAGTAATCTCACTCAAGCTATTTATAC	540
OY	659	ATCTCCACTGTATCTATTAACAAGTGGCAAGAATACTTGTTTGGTCCAGCAGCAAC	718
Db	541	ATCTCCACTGTATCTATTAACAAGTGGCAAGAATACTTGTTTGGTCCAGCAGCAAC	600
OY	719	GCACTAGGCAATGSAAGATCAAAACAACTGCAAAATTCACCTGGATGATATATGATACT	778
Db	601	GCACTAGGCAATGSAAGATCAAAACAACTGCAAAATTCACCTGGATGATATATGATACT	660
OY	779	TCTGAGCGCTCATTTCCAGGGCTGAGACTAATATGTACAGTGCACCAAGCCATAATT	838
Db	661	TCTGAGCGCTCATTTCCAGGGCTGAGACTAATATGTACAGTGCACCAAGCCATAATT	720
OY	839	TATTTGGATAGTCAAAACAACAATTGAAAGGTTTCTGTGAATGATATCAGGCTACA	898
Db	721	TATTTGGATAGTCAAAACAACAATTGAAAGGTTTCTGTGAATGATATCAGGCTACA	780
OY	899	ACAAACCAACCTTGGAAATGTTAAAGATTGACACCAATTTTACATATGTGCAACAGCA	958
Db	781	ACAAACCAACCTTGGAAATGTTAAAGATTGACACCAATTTTACATATGTGCAACAGCA	840
OY	959	GAATTTCACTTGGAGCCAAACATTAAGTACGTAATTTCAAGTGAATGTCAGAAACAGGC	1018
Db	841	GAATTTCACTTGGAGCCAAACATTAAGTACGTAATTTCAAGTGAATGTCAGAAACAGGC	900
OY	1019	AAAAGATCTGGCAGCCTTGGAGTTCACCGTTTTTCAATAAACCTGAAACAGTTCCTC	1078
Db	901	AAAAGATCTGGCAGCCTTGGAGTTCACCGTTTTTCAATAAACCTGAAACAGTTCCTC	960
OY	1079	CAGGTCACATCAAAAGCAATTCCAACATGACACATGGAATTTCTGGGCTAACAGTTGCTTC	1138
Db	961	CAGGTCACATCAAAAGCAATTCCAACATGACACATGGAATTTCTGGGCTAACAGTTGCTTC	1020
OY	1139	ATCTCTACAGGACCTTACTTCTGACAAACAGAGGACATTTGACCTTTATTTGGAAATG	1198
Db	1021	ATCTCTACAGGACCTTACTTCTGACAAACAGAGGACATTTGACCTTTATTTGGAAATG	1080
OY	1199	ATCGCTTTGCTGTATATGTGCAATTCCTTCTTGTATTTGGATTTTAAACAAGATCATTC	1258
Db	1081	ATCGCTTTGCTGTATATGTGCAATTCCTTCTTGTATTTGGATTTTAAACAAGATCATTC	1140

QY	1259	GGAACGTGGATTAATAAGAGGACTCTTAATGTGTAATACCAAGGTGGCTTATGAAGAATAT	13.18
Db	1141	CGAATCGGGATTTAAAGAGAGATCTTAATGTGTAATACCAAGGTGGCTTATGAAGAATAT	1200
QY	1319	CCTAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGAAAAATAGTGAATTATGAT	13.78
Db	1201	CCTAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGAAAAATAGTGAATTATGAT	1260
QY	1379	AATTAATTCGAGTGGCAGGTCTTAATGTGTAATCCCATGATTAACAGAGATTAAGAAAAATC	143.8
Db	1261	AATTAATTCGAGTGGCAGGTCTTAATGTGTAATCCCATGATTAACAGAGATTAAGAAAAATC	1320
QY	1439	TTGATCCGAGAACCAAGCCTTACAGACTACAAAGAGAGAAATACAGAGCCCTGGAGACA	149.8
Db	1321	TTGATCCGAGAACCAAGCCTTACAGACTACAAAGAGAGAAATACAGAGCCCTGGAGACA	1380
QY	1499	AGAGACTACCCGCAAAACTCGCTATTGCAACATCTACAGTTGTATATATTCCTGATCTC	155.8
Db	1381	AGAGACTACCCGCAAAACTCGCTATTGCAACATCTACAGTTGTATATATTCCTGATCTC	1440
QY	1559	AACACTGGATTTAAACCCCAATTTCAAATTTTCGCTGAGGGAAGCCATCTCAGCAAT	161.8
Db	1441	AACACTGGATTTAAACCCCAATTTCAAATTTTCGCTGAGGGAAGCCATCTCAGCAAT	1500
QY	1619	AATATATGAAATTACTTCCTTAACTTAACCTTAACCAACAGTGAATTCCTTAAGACTCAGAAAT	167.8
Db	1501	AATATATGAAATTACTTCCTTAACTTAACTTAACCAACAGTGAATTCCTTAAGACTCAGAAAT	1560
QY	1679	AATCCCAAGTTACAAAAGCAATCTTAATTTGCTTTTCTGTTTCAGGTGAAATTCACTA	173.8
Db	1561	AATCCCAAGTTACAAAAGCAATCTTAATTTGCTTTTCTGTTTCAGGTGAAATTCACTA	1620
QY	1739	AGCAACACAATATTTCTTGAGAAATTAAGCTCATTAATTAATCAAGAGAAATGCAATTCCT	179.8
Db	1621	AGCAACACAATATTTCTTGAGAAATTAAGCTCATTAATTAATCAAGAGAAATGCAATTCCT	1680
QY	1799	CCCTACATATCAAACTCAGTAGAGAGAGAAAAACACATAGCTTTTGAAAAATGATTCACCC	185.8
Db	1681	CCCTACATATCAAACTCAGTAGAGAGAGAAAAACACATAGCTTTTGAAAAATGATTCACCC	1740
QY	1859	AGTGAATATATTCAGAACAGAGCCCTGCTTCCTGATGAATTTGTCCTGTGTTGGGATC	191.8
Db	1741	AGTGAATATATTCAGAACAGAGCCCTGCTTCCTGATGAATTTGTCCTGTGTTGGGATC	1800
QY	1919	GTCGATAGAGAGTTGCCATCTATTAAATCTTAATTTTCCAAAAATATTTTGAAAGCCAC	197.8
Db	1801	GTCGATAGAGAGTTGCCATCTATTAAATCTTAATTTTCCAAAAATATTTTGAAAGCCAC	1860
QY	1979	TTCAATATGAAATTTCACTCTTGAAAAATAGAGAGCTGTGTGTGCAAAATTCAA	202.8
Db	1861	TTCAATATGAAATTTCACTCTTGAAAAATAGAGAGCTGTGTGTGCAAAATTCAA	1910

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1  RESULT 10
2  US-09-972-708-20
3  Sequence 20. Application US/09972708
4  Publication No US20030059871A1
5  GENERAL INFORMATION:
6  APPLICANT: Immunex Corporation
7  APPLICANT: Cosman, David J.
8  APPLICANT: Mosley, Bruce A.
9  APPLICANT: Bird, Timothy A.
10 APPLICANT: Dubose, Robert F.
11 APPLICANT: Wiley, Steven R.
12 TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HP1 AND HP2
13 FILE REFERENCE: 3160-B
14 CURRENT APPLICATION NUMBER: US/09/972,708
15 CURRENT FILING DATE: 2001-10-05
16 NUMBER OF SEQ ID NOS: 29
17 SOFTWARE: PatentIn version 3.1
18 SEQ ID NO 20
19 LENGTH: 1690
20 TYPE: DNA

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ORGANISM: Homo sapiens
US-09-972-708-20

66.1%; Score 1887.6; DB 3; Length 1890;

Query Match Best Local Similarity 99.8%; Pred. No. 0;

Matches 1887; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 ATGAAATGAGTCACTATTCATAGGAGATGAGTATAGCCCTTTTACATACCTTTCAGCTGG 178
DB 1 ATGAAATGAGTCACTATTCATAGGAGATGAGTATAGCCCTTTTACATACCTTTCAGCTGG 60
QY 179 TGTGATGAGGAAATTAACAATATTAACCTGCTTGCCCAATCTGGGTAGAACGACCA 238
DB 61 TGTGATGAGGAAATTAACAATATTAACCTGCTTGCCCAATCTGGGTAGAACGACCA 120
QY 239 ATTTTAAAGTGGTATGAATATCTATATATTTGGCCAGAGAAATTAAGAACTGGCAA 298
DB 121 ATTTTAAAGTGGTATGAATATCTATATATTTGGCCAGAGAAATTAAGAACTGGCAA 180
QY 299 CCAAGGAAATCTTATTTTATTAATAATGCGATCAAGAGAAATTTCAAAATCAAGAGATT 358
DB 181 CCAAGGAAATCTTATTTTATTAATAATGCGATCAAGAGAAATTTCAAAATCAAGAGATT 240
QY 359 AATTAACAACAAGCTCGGCTTTGGTATTAATACTTTGGAACCAATGCTTCTATGTAC 418
DB 241 AATTAACAACAAGCTCGGCTTTGGTATTAATACTTTGGAACCAATGCTTCTATGTAC 300
QY 419 TGCATGCTGATATGCTCCCAACATTTTCAAGAGACATGATATGTGAAAAGACATTTCT 478
DB 301 TGCATGCTGATATGCTCCCAACATTTTCAAGAGACATGATATGTGAAAAGACATTTCT 360
QY 479 TCTGATATGCGGACAGATATCTGATGAAGTAACTGTGATTTATTAATATTTAGG 538
DB 361 TCTGATATGCGGACAGATATCTGATGAAGTAACTGTGATTTATTAATATTTAGG 420
QY 539 AACATGACTTGACCTGGAATGCTGGAGAGCTCACTAACAATGACAAATAATGCTG 598
DB 421 AACATGACTTGACCTGGAATGCTGGAGAGCTCACTAACAATGACAAATAATGCTG 480
QY 599 CATGTGAAGGTTTGAAGACAGAAAGAGACAAAGATATCTCACTCAAGTATATTTAC 658
DB 481 CATGTGAAGGTTTGAAGACAGAAAGAGACAAAGATATCTCACTCAAGTATATTTAC 540
QY 659 ATCTCCACTGATTAACAAGTGGCAAGAGATGCTGTTGGGTCCAAAGCAAGAAC 718
DB 541 ATCTCCACTGATTAACAAGTGGCAAGAGATGCTGTTGGGTCCAAAGCAAGAAC 600
QY 719 GCACTAGGATGGAAGATCAAAACAATGCAAAATTCACCTGATGATATAGTATCCT 778
DB 601 GCACTAGGATGGAAGATCAAAACAATGCAAAATTCACCTGATGATATAGTATCCT 660
QY 779 TCTGACACCGCTCATTTCCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACATATT 838
DB 661 TCTGACACCGCTCATTTCCAGGGCTGAGACTATTAATGCTACAGTCCCAAGACATATT 720
QY 839 TATTTGGATATGCTAAACAATGGAAGGTTTCTGTGAAATGAAATCAAGGCTACA 898
DB 721 TATTTGGATATGCTAAACAATGGAAGGTTTCTGTGAAATGAAATCAAGGCTACA 780
QY 899 ACAAAACCAAACTTGAATGTTAAAGAAATTTGACCAATTTTACATATGTGCAACATCA 958
DB 781 ACAAAACCAAACTTGAATGTTAAAGAAATTTGACCAATTTTACATATGTGCAACATCA 840
QY 959 GAATTTACTTGGAGCCAAACATTAAGTATGATTTCAAGTGAATGCAAGAAACGCG 1018
DB 841 GAATTTACTTGGAGCCAAACATTAAGTATGATTTCAAGTGAATGCAAGAAACGCG 900
QY 1019 AAAAGTACTGCGACCTTGGAGTCAACGTTTTCATATAAACCCTGAAACAGTTCCC 1078
DB 901 AAAAGTACTGCGACCTTGGAGTCAACGTTTTCATATAAACCCTGAAACAGTTCCC 960
QY 1079 CAGGTCAATCAAAAGATTCACATGACATGAAATCTGGGCTTACAGTTGCTTCC 1138

DB 961 CAGGTCAATCAAAAGATTCACATGACATGAAATCTGGGCTTACAGTTGCTTCC 1020
QY 1139 ATCTTACAGGAGACCTTACTTCTGACAAAGAGAGACATATGGAATTTATTTGGGAATG 1198
DB 1021 ATCTTACAGGAGACCTTACTTCTGACAAAGAGAGACATATGGAATTTATTTGGGAATG 1080
QY 1199 ATGCTTTTCTGTATATGTTGTCAATTCCTTTTGTGATTTGGATATTTAACAGATCAATC 1258
DB 1081 ATGCTTTTCTGTATATGTTGTCAATTCCTTTTGTGATTTGGATATTTAACAGATCAATC 1140
QY 1259 CGAACTGGGATTTAAAGAGATCTTATTTGTATATACCAAGTGGCTTTATGAAGATTT 1318
DB 1141 CGAACTGGGATTTAAAGAGATCTTATTTGTATATACCAAGTGGCTTTATGAAGATTT 1200
QY 1319 CTTATATGAAATAACAGCAATGTTGTGAATGCTACAGGAAATAATGAACTTATGAAAT 1378
DB 1201 CTTATATGAAATAACAGCAATGTTGTGAATGCTACAGGAAATAATGAACTTATGAAAT 1260
QY 1379 AATTAATTCAGTGAAGCAGGTCTATATATGTTGATCCATGATTTACAGAGATTAAGAAATC 1438
DB 1261 AATTAATTCAGTGAAGCAGGTCTATATATGTTGATCCATGATTTACAGAGATTAAGAAATC 1320
QY 1439 TTGATCCAGAACCAAGCCTTACAGACTTACAGAGAGAAATACAGAACCCCTGAGACA 1458
DB 1321 TTGATCCAGAACCAAGCCTTACAGACTTACAGAGAGAAATACAGAACCCCTGAGACA 1380
QY 1499 AGAGACTACCCGAGAAACCTGCTATTTGCAATATCTACAGTATATATTTCTGATCTC 1558
DB 1381 AGAGACTACCCGAGAAACCTGCTATTTGCAATATCTACAGTATATATTTCTGATCTC 1440
QY 1559 AACACTGATATTAACCCCAAAATTTTCAATTTTCTGCTGAGGAGAACCACTTCAGCAAT 1618
DB 1441 AACACTGATATTAACCCCAAAATTTTCAATTTTCTGCTGAGGAGAACCACTTCAGCAAT 1500
QY 1619 AATTAATGAATTAATCTTCTTAACTTAACCTTAACCAACAGTATTTCTTGAATCTGAGAAAT 1678
DB 1501 AATTAATGAATTAATCTTCTTAACTTAACCAACAGTATTTCTTGAATCTGAGAAAT 1560
QY 1679 AATCCAGGTTACAAAGGATCCGAATTTTGTGCTTTTCTGTTTCAAGTGAATTTCACTA 1738
DB 1561 AATCCAGGTTACAAAGGATCCGAATTTTGTGCTTTTCTGTTTCAAGTGAATTTCACTA 1620
QY 1739 AGCAACAATATTTCTTGGAGATTAAGCCTCATATTAATCAAGAGAAATGCAATCT 1798
DB 1621 AGCAACAATATTTCTTGGAGATTAAGCCTCATATTAATCAAGAGAAATGCAATCT 1680
QY 1799 CTTGACATCAAAAATCTAGTGAAGAGAGAAACCAACATGCTTTTGGAAAATGATTCACC 1858
DB 1681 CTTGACATCAAAAATCTAGTGAAGAGAGAAACCAACATGCTTTTGGAAAATGATTCACC 1740
QY 1859 AGTGAACCTATTTCCAGAAACGAGACCTGCTTCCGATGAATTTGTCTCTGTTGGGGATC 1918
DB 1741 AGTGAACCTATTTCCAGAAACGAGACCTGCTTCCGATGAATTTGTCTCTGTTGGGGATC 1800
QY 1919 GTGAATGAGAGTTGCCATCTATTAATCTTATTTTCCAAAATATTTTGGAAAGCAC 1978
DB 1801 GTGAATGAGAGTTGCCATCTATTAATCTTATTTTCCAAAATATTTTGGAAAGCAC 1860
QY 1979 TTCAATGAGATTTCACTTTTGGAAAAGTAG 2008
DB 1861 TTCAATGAGATTTCACTTTTGGAAAAGTAG 1890

RESULT 11
US-10-715-667-20
; Sequence 20, Application US/10715667
; Publication No. US20040152161A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.

; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
 ; FILE REFERENCE: 3160-B
 ; CURRENT APPLICATION NUMBER: US/10/715,667
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: US/09/972,708
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 1890
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-715-667-20

Query Match 66.1%; Score 1887.6; DB 8; Length 1890;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1887; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 ATGAATCAGTCACTATTCATAGGATGAGTAATAGCCCTTTACATACCTTCACTG 178
 DB 1 ATGAATCAGTCACTATTCATAGGATGAGTAATAGCCCTTTACATACCTTCACTG 60
 QY 179 TGTCAATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 238
 DB 61 TGTCAATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 QY 239 ATTTTATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 298
 DB 121 ATTTTATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180
 QY 299 CCAAGGAACTTCAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 358
 DB 181 CCAAGGAACTTCAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
 QY 359 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 418
 DB 241 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 QY 419 TGCATGCTGATATGCTCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 478
 DB 301 TGCATGCTGATATGCTCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 QY 479 TGTGATATCCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 538
 DB 361 TGTGATATCCGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 QY 539 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 598
 DB 421 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
 QY 599 CATGTAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 658
 DB 481 CATGTAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
 QY 659 ATCTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 718
 DB 541 ATCTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 QY 719 GCACTAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 778
 DB 601 GCACTAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 660
 QY 779 TGTGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 838
 DB 661 TGTGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
 QY 839 TATTTGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 898
 DB 721 TATTTGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 780
 QY 899 ACAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 958

DB 781 ACAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 QY 959 GAATTTACTGAGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1018
 DB 841 GAATTTACTGAGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 QY 1019 AAAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1078
 DB 901 AAAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
 QY 1079 CAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1138
 DB 961 CAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
 QY 1139 ATCTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1198
 DB 1021 ATCTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
 QY 1199 ATCTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1258
 DB 1081 ATCTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
 QY 1259 CGAATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1318
 DB 1141 CGAATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1200
 QY 1319 CCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1378
 DB 1201 CCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1260
 QY 1379 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1438
 DB 1261 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
 QY 1439 TTCATCCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1498
 DB 1321 TTCATCCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1380
 QY 1499 AGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1558
 DB 1381 AGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
 QY 1559 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1618
 DB 1441 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
 QY 1619 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1678
 DB 1501 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
 QY 1679 AATCCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1738
 DB 1561 AATCCAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
 QY 1739 AGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1798
 DB 1621 AGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
 QY 1799 CTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1858
 DB 1681 CTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
 QY 1859 AGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1918
 DB 1741 AGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
 QY 1919 GTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1978
 DB 1801 GTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
 QY 1979 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2008
 DB 1861 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1890

Db 1549 AGTGAAGAGTTTGAAGACAGAGACAGACCTGCTTCGATGATTAATTCCTGCTGGGGATC 1608
Qy 1919 GTGAATGAGAGTTGCGATCATCTATTAATCTATTTTCCAAAATTTTGGAAAGCCAC 1978
Db 1609 GTGAATGAGAGTTGCGATCATCTATTAATCTATTTTCCAAAATTTTGGAAAGCCAC 1668
Qy 1979 TTCAATGAGATTTCACTCTTGGAAAAGTAG 2008
Db 1669 TTCAATGAGATTTCACTCTTGGAAAAGTAG 1698

RESULT 13
US-10-715-667-22
Sequence 22, Application US/10715667
Publication No. US20040152161A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/10/715,667
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/09/972,708
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 1698
TYPE: DNA
ORGANISM: Homo sapiens
US-10-715-667-22

Query Match 52.3%; Score 1493.6; DB 8; Length 1698;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 1699; Conservative 2; Mismatches 1; Indels 192; Gaps 1;

Qy 119 ATGATACATGCTCACTATTCATGAGATGCGATTAATAGCCCTTTACATCTCTTCAAGTGG 178
Db 1 ATGATACATGCTCACTATTCATGAGATGCGATTAATAGCCCTTTACATCTCTTCAAGTGG 60
Qy 179 TGTGATGAGAGATTAACAATATTAATGCTGCGGACCAATCGGATGAGAACGAGCCACA 238
Db 61 TGTGATGAGAGATTAACAATATTAATGCTGCGGACCAATCGGATGAGAACGAGCCACA 120
Qy 239 ATTTTAAAGTGGATGAATATCTCTATATATTTGCCAAGCAGCAATTAAGAACTGCCAA 298
Db 121 ATTTTAAAGTGGATGAATATCTCTATATATTTGCCAAGCAGCAATTAAGAACTGCCAA 180
Qy 299 CCAAGGAACTTCAATTTTAAATAATGCGATCAAGAAAGATTTCAATATCAAGGATT 358
Db 181 CCAAGGAACTTCAATTTTAAATAATGCGATCAAGAAAGATTTCAATATCAAGGATT 240
Qy 359 AATPAAACAAGCTGGCTTGGTATAAAAATTTTGGAAACCAATGCTTCAATGATAC 418
Db 241 AATPAAACAAGCTGGCTTGGTATAAAAATTTTGGAAACCAATGCTTCAATGATAC 300
Qy 419 TGCATGCTGAATGTCCTCAAAATTTTCAAGAGACATGATATGTAAGAAAGCAATTTCT 478
Db 301 TGCATGCTGAATGTCCTCAAAATTTTCAAGAGACATGATATGTAAGAAAGCAATTTCT 360
Qy 479 TCTGATATCCGCCAGATATCTGATGAAGTAACCTGTGCTATTAATGAATATTCAGGC 538
Db 361 TCTGATATCCGCCAGATATCTGATGAAGTAACCTGTGCTATTAATGAATATTCAGGC 420
Qy 539 AATGATGCTGACCTGGAATGCTGGAAGCTGACCTCAATGACAAATAATCGTGTA 598
Db 421 AATGATGCTGACCTGGAATGCTGGAAGCTGACCTCAATGACAAATAATCGTGTA 480

Qy 599 CATGGAAGAGTTTGAAGACAGAAAGAGCAACAGATATCTCACTCCAAAGCTATATTAAC 658
Db 481 CATGGAAGAGTTTGAAGACAGAAAGAGCAACAGATATCTCACTCCAAAGCTATATTAAC 540
Qy 659 ATCTGCACTGATTCATTAACAAGTGGCAAGAAAGTACTGTTGGTTCGAAGAGCAAC 718
Db 541 ATCTGCACTGATTCATTAACAAGTGGCAAGAAAGTACTGTTGGTTCGAAGAGCAAC 600
Qy 719 GCATGAGGATGGAAGAGTCAAAACAATGCAAAATTCACCTGATATATAGTATACCT 778
Db 601 GCATGAGGATGGAAGAGTCAAAACAATGCAAAATTCACCTGATATATAGTATACCT 660
Qy 779 TCTGACCGGTCATTTCCAGGCTGAGACTATTAATGCTACAGTCCCAAGACATTAAT 838
Db 661 TCTGACCGGTCATTTCCAGGCTGAGACTATTAATGCTACAGTCCCAAGACATTAAT 720
Qy 839 TATTTGGATATGTCAAACAATTAAGAAAGTTTCTGTGAATGAGATTAACAAGCTACA 898
Db 721 TATTTGGATATGTCAAACAATTAAGAAAGTTTCTGTGAATGAGATTAACAAGCTACA 780
Qy 899 ACAAAACAACTGGAATGTTAAAGATTTGACACCAATTTTACATATGTCACACAGTCA 958
Db 781 ACAAAACAACTGGAATGTTAAAGATTTGACACCAATTTTACATATGTCACACAGTCA 840
Qy 959 GAAATTTACTTGGAGCCAAACATTAAGTACGTAATTTCAAGTGAATGTCACAAAGGC 1018
Db 841 GAAATTTACTTGGAGCCAAACATTAAGTACGTAATTTCAAGTGAATGTCACAAAGGC 900
Qy 1019 AAAAGTACTGGAAGCTTGGAGTTGACCGTTTTCATTAACACTGAAACAGTTCC 1078
Db 901 AAAAGTACTGGAAGCTTGGAGTTGACCGTTTTCATTAACACTGAAACAGTTCC 954
Qy 1079 CAGTGCATCAAAAGCATTCACACATGACACATGGAATTTGGCTAACAGTTGCTCC 1138
Db 955 ----- 954
Qy 1139 ATCTTAAGAGGACCTTACTCTGACAAACAGAGAGACATTTGACTTTATGGAAATG 1198
Db 955 ----- 954
Qy 1199 ATGCTCTTGGCTATATGTTGTCATTTCTTTGATTGGGATATTTAACAGATCATTC 1258
Db 955 ----- 954
Qy 1259 CGAATGGATTAAGAAAGAGATCTTATGTTAATCAAAAGTGGCTTATGAAAGATTT 1318
Db 955 -----GGAATTAAGAAAGAGATCTTATGTTAATCAAAAGTGGCTTATGAAAGATTT 1008
Qy 1319 CCTAATATGAAAAACAGCAATGTTGAAATGCTACAGGAAATATGTAATGTAAT 1378
Db 1009 CCTAATATGAAAAACAGCAATGTTGAAATGCTACAGGAAATATGTAATGTAAT 1068
Qy 1379 AATPATTCCAGTGAAGAGGCTATATGTTGATCCCATGATTAACAAGATTAAGAAATC 1438
Db 1069 AATPATTCCAGTGAAGAGGCTATATGTTGATCCCATGATTAACAAGATTAAGAAATC 1128
Qy 1439 TTGATCCCAAGAACACAAAGCTTACAGACTACAAAGAAAGATACAGAACCCCTGAGACA 1498
Db 1129 TTGATCCCAAGAACACAAAGCTTACAGACTACAAAGAAAGATACAGAACCCCTGAGACA 1188
Qy 1499 AGAGACTACCCGAAATCTGCTATTTGACATATCAAGTTGATATATCTGATCTC 1558
Db 1189 AGAGACTACCCGAAATCTGCTATTTGACATATCAAGTTGATATATCTGATCTC 1248
Qy 1559 AACAATGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCAGCAAT 1618
Db 1249 AACAATGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCAGCAAT 1308
Qy 1619 AATPAAATTAATCTTCTTAAACATTAACACCAAGTTGATCTTAACTGAGAAAT 1678
Db 1309 AATPAAATTAATCTTCTTAAACATTAACACCAAGTTGATCTTAACTGAGAAAT 1368
Qy 1679 AATCCAGGTTTACAAAGATCTTAATTTTGTCTTTTCTGTTCAGATGTAATTCATCA 1738

Db 1369 AATCCAGGTACAAAGCATCTTAATTTGCTTTCTGTTCAAGTGAATTCACCTA 1428
Qy 1739 AGCAACCAATATTTCTTGGAGAAATTAAGCTCAATTAATTAAGAGAAATGCAATTC 1798
Db 1429 AGCAACCAATATTTCTTGGAGAAATTAAGCTCAATTAATTAAGAGAAATGCAATTC 1488
Qy 1799 CCGACATACAAACCTAGTAAAGAGAGAAACCAACATGCTTTTGGAAAAATGATTCACC 1858
Db 1489 CCGACATACAAACCTAGTAAAGAGAGAAACCAACATGCTTTTGGAAAAATGATTCACC 1548
Qy 1859 AGTGAACCTATTCAGAAAGACACCTGCTTCTGTAATTAATTTGCTGTTGGGGATC 1918
Db 1549 AGTGAACCTATTCAGAAAGACACCTGCTTCTGTAATTAATTTGCTGTTGGGGATC 1608
Qy 1919 GTGAATGAGAGATTCATCTATTAATTAATTTTTCACAAAATTTTGGAAAGCCAC 1978
Db 1609 GTGAATGAGAGATTCATCTATTAATTAATTTTTCACAAAATTTTGGAAAGCCAC 1668
Qy 1979 TTCAATGATTCATCTGTTGAAAGTAG 2008
Db 1669 TTCAATGATTCATCTGTTGAAAGTAG 1698
RESULT 14
US-10-105-930-3
; Sequence 3, Application US/10105930
; Publication No. US2003009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatatsu
; TITLE OF INVENTION: NOVEL HEMOPROTEIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105U1
; CURRENT APPLICATION NUMBER: US/10/105, 930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98)...(1381)
US-10-105-930-3
Query Match 46.3%; Score 1322.8; DB 6; Length 1479;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1324; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 28 CAGCCAAAGAGGCTGAGAGCTGCTGTGAAGTGAATTAATGCTTCAAGAGTTGAA 87
Db 7 CAGCCAAAGAGGCTGAGAGCTGCTGTGAAGTGAATTAATGCTTCAAGAGTTGAA 66
Qy 88 AGAGGAGAAAGCTTTTCTGCTTCAGACATGAATCACTATTCATTAAGGATGC 147
Db 67 AGAGGAGAAAGCTTTTCTGCTTCAGACATGAATCACTATTCATTAAGGATGC 126
Qy 148 AGTAATAGCCCTTTACATCTCTTCACTGCTGTGATGAGAAATTAATAATTAATC 207
Db 127 AGTAATAGCCCTTTACATCTCTTCACTGCTGTGATGAGAAATTAATAATTAATC 186
Qy 208 CTTGCGCAATCTGGGTAAACAGCAATTTTAAATGGTATGAATCTCTAT 267
Db 187 CTTGCGCAATCTGGGTAAACAGCAATTTTAAATGGTATGAATCTCTAT 246
Qy 268 ATATTGCCAAGCAATTAAGAACTGCCAAGCAAGAACTTATTTTAAATG 327

Db 247 ATATTGCCAAGCAATTAAGAACTGCCAAGCAAGAACTTATTTTAAATG 306
Qy 328 CATCAAGAAAGATTTCAATTCAGAGATTAATTAACAAAGCTGGCTTGTATA 387
Db 307 CATCAAGAAAGATTTCAATTCAGAGATTAATTAACAAAGCTGGCTTGTATA 366
Qy 388 AACTTTCTGGAACCAATGCTTCTATGTCTGCACTGTGAATGTGCCAAATTTCA 447
Db 367 AACTTTCTGGAACCAATGCTTCTATGTCTGCACTGTGAATGTGCCAAATTTCA 426
Qy 448 AGAGACATGATATGTGAAAGAAACATTTCTGTGATATCCGACATATTCCTATGA 507
Db 427 AGAGACATGATATGTGAAAGAAACATTTCTGTGATATCCGACATATTCCTATGA 486
Qy 508 AGTAACCTGTGATTAATTAATTAATTTCAAGCAATGACCTTGAATGTGTGAA 567
Db 487 AGTAACCTGTGATTAATTAATTAATTTCAAGCAATGACCTTGAATGTGTGAA 546
Qy 568 GCTCACCCTACATGACCAAAATACGTGTGATACATGTAAGAGTTAGACAGAAAGA 627
Db 547 GCTCACCCTACATGACCAAAATACGTGTGATACATGTAAGAGTTAGACAGAAAGA 606
Qy 628 GCAACAGTATCTCAGCTCAAGCTATATTAATTCATCTCAGTATTCATTAAGGTGCA 687
Db 607 GCAACAGTATCTCAGCTCAAGCTATATTAATTCATCTCAGTATTCATTAAGGTGCA 666
Qy 688 GAAATCTGTTGGGTCCAGCAGCAACGCACTAGGATGGAAGATCAAAACACT 747
Db 667 GAAATCTGTTGGGTCCAGCAGCAACGCACTAGGATGGAAGATCAAAACACT 726
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; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030009018A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/jp00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1284)
US-10-105-930-7

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Job time : 3012 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 12:25:14 ; Search time 15913 Seconds
(without alignments)
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Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb om:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	2824.4	98.8	2826	5	AF461422 Homo sapi
6	2810.2	98.3	2830	2	AX467349 Sequence
7	2081.4	72.8	2123	2	BD013243 Novel hem
8	1906	66.7	1910	2	BD013245 Novel hem
9	1887.6	66.1	1890	2	AX467350 Sequence
10	1773.8	62.1	1779	5	AY937250 Homo sapi
11	1556.2	54.5	1676	5	AY937253 Homo sapi
12	1505.2	52.7	12289	5	AY937254 Homo sapi
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14	1440.2	50.4	1618	5	AY937251 Homo sapi
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21	1236.6	43.3	1301	2	BD013244 Novel hem
22	1213.6	42.5	1324	5	BC016829 Homo sapi
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25	1105.8	38.7	1935	2	AX467359 Sequence
26	1043.4	36.5	1071	2	AX467354 Sequence
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31	375	13.1	235198	12	AC106222 Rattus no
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	CDS
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mat_peptide

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS CS110317
DEFINITION Sequence 1 from Patent WO2005052157.
ACCESSION CS110317
VERSION CS110317.1 GI:68148524
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homiidae; Homo.
REFERENCE
    1 Chirica, M., Kastelein, R.A., Moore, K.W. and Parham, C.L.
    IL-23 and its receptor: related reagents and methods
    Patent: WO 2005052157-A 1 09-JUN-2005;
    Schering Corporation (US)
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DEFINITION Sequence 1 from patent US 6756481.
ACCESSION AR561607
VERSION AR561607.1 GI:53974707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2859)
AUTHORS Chirica, M., Kastelein, R.A., Moore, K.W. and Parham, C.L.
TITLE IL-23 receptor binding compositions
JOURNAL Patent: US 6756481-A 1 29-JUN-2004;
Scherling Corporation; Kenilworth, NJ
FEATURES
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LOCUS	AX338549	2859 bp	DNA	linear	PAT 09-JAN-2002
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VERSION	AX338549.1				
KEYWORDS	GI:18128949				
SOURCE	unidentified				
ORGANISM	unclassified sequences.				
REFERENCE	1				
AUTHORS	Chirica, M., Kaebele, R. A., Moore, K. W. and Parham, C. L.				
TITLE	Mammalian receptor proteins; related reagents and methods				
JOURNAL	Patent: WO 0185790-A 1 15-NOV-2001;				
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ACCESSION AF61422.1 GI:21239251
VERSION
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Homidae; Homo.
1 (bases 1 to 2826)
Barham, C., Chirica, M., Timans, J., Vaisberg, E., Travis, M.,
Cheung, U., Pflanz, S., Zhang, R., Singh, K.P., Vega, F., To, W.,
Wagner, U., O'Farrell, A.-M., McClanahan, T., Zurawski, S., Hannum, C.,
Gorman, D., Rennick, D.M., Kastelein, R.A., de Waal Malefyt, R. and
Moore, K.W.
A receptor for the heterodimeric cytokine IL-23 is composed of
IL-12beta1 and a novel cytokine receptor subunit, IL-23R
J. Immunol. 168 (11), 5699-5708 (2002)
12023369
2 (bases 1 to 2826)
Barham, C., Chirica, M., Timans, J., Vaisberg, E., Travis, M.,
Cheung, U., Pflanz, S., Zhang, R., Singh, K.P., Vega, F., To, W.,
Wagner, U., O'Farrell, A.-M., McClanahan, T., Zurawski, S., Hannum, C.,
Gorman, D., Rennick, D.M., Kastelein, R.A., de Waal Malefyt, R. and
Moore, K.W.
Direct Submission
Submitted (19-DEC-2001) Immunology, DNAX Research, 901 California
Ave., Palo Alto, CA 94304, USA
FEATURES
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 ORGANISM Homo sapiens
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 Homidae; Homo.
 REFERENCE 1

AUTHORS Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
TITLE Hematopoietin receptors hprt1 and hprt2
JOURNAL Patent: WO 0229060-A 19 11-APR-2002;
Immunex Corporation (US)
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Qy	2128	ACATGGAACACATGTTTTTCAATTCCTTGGATTAATACCTAGATGAGGATTTGCTGGCCA	2187
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Qy	2248	CTCCTACCATGACCAATGTAAGAAATTCGCGGAGCTCCATGCTTTTAAATTTAGCCATT	2307
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Qy	2668	ACCTGTGCTCACTAAATTAATTAACCCGCGCATATGTGTGAGAGTGTCTGTAAATCC	2727
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RESULT 7			
BD013243		2123 bp	DNA linear
LOCUS	BD013243		
DEFINITION	Novel hemopoietin receptor protein, NR12.		
ACCESSION	BD013243.1	GI:22094932	
VERSION	WO 0123556-A/3.		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2123)		
TITLE	Maeda, M. and Yaguchi, N.		
	Novel hemopoietin receptor protein, NR12		

JOURNAL	Patent: WO 0123556-A 3 05-Apr-2001; CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC., ASATSUGU MAEDA, NORIKO YAGUCHI											
COMMENT	OS Homo sapiens (human) PN WO 0123556-A/3											
FEATURES	CC FH Key Location/Qualifiers FT CDS (98) . . (1984) . SOURCE location/Qualifiers 1. .2123 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"											
ORIGIN	Query Match 72.8%; Score 2081.4; DB 2; Length 2123; Best Local Similarity 99.5%; Pred. No. 0; Matches 2085; Conservative 2; Mismatches 8; Indels 0; Gaps 0;											
Oy	28	CAGCCAA	CAAGGGG	GGAGG	CTGGCTCTG	AAGTGA	ATTATG	TGCTTCA	CAACAG	TTGAA	87	
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Oy	88	AGAGG	AAACAGTCTTTT	CTGCTT	CCAGCATG	GAATCA	GTCACTA	TTCAAT	TGAGATG	C	147	
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 LOCUS BD013245 1910 bp DNA linear PAT 02-AUG-2002
 DEFINITION Novel hemopoietin receptor protein, NR12.
 ACCESSION BD013245
 VERSION BD013245.1 GI:22093434
 KEYWORDS MO 0123556-A/5.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 1910)
 AUTHORS Maeda,M. and Yaguchi,N.
 TITLE Novel hemopoietin receptor protein, NR12
 JOURNAL Patent: WO 0123556-A 5 05-APR-2001;
 CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, ASATSUGU
 MAEDA, NORIKO YAGUCHI
 COMMENT OS Homo sapiens (human)
 PN MO 0123556-A/5
 PD 05-APR-2001
 PR 27-SEP-2000 WO 2000JP006654
 PR 27-SEP-1999 JP 99P 273358, 03-AUG-2000 JP 00P 240397 PI
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 PC C12N15/12, C12N1/21, C12N5/10, C07K14/715, C07K16/28, C12P21/02, PC
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 Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 1779)
 AUTHORS Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
 Wang,S.H. and Liu,L.
 TITLE Identification and expression analysis of alternatively spliced
 isoforms of human interleukin-23 receptor gene in normal lymphoid
 cells and selected tumor cells

JOURNAL Immunogenetics 57 (12), 934-943 (2006)
PUBMED 16372191
REFERENCE 2 (bases 1 to 1779)
AUTHORS Zhang, X.-Y., Zhang, Y., Wang, S.-H. and Liu, L.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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DEFINITION cds, alternatively spliced.
ACCESSION AY937253
VERSION AY937253.1 GI:62870704
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ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Zhang, X.Y., Zhang, Y., Zhang, H.J., Fu, Y.J., He, J., Zhu, L.P.,
Wang, S.H. and Liu, L.
TITLE Identification and expression analysis of alternatively spliced
isoforms of human interleukin-23 receptor gene in normal lymphoid
cells and selected tumor cells
JOURNAL Immunogenetics 57 (12), 934-943 (2006)
PUBMED 16372191
REFERENCE 2 (bases 1 to 1676)
AUTHORS Zhang, X.-Y., Zhang, Y., Zhang, H.-J., Wang, S.-H. and Liu, L.
TITLE Direct Submision
JOURNAL Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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 1 (bases 1 to 1676)
 Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
 Wang,S.H. and Liu,L.
 Identification and expression analysis of alternatively spliced
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 Immunogenetics 57 (12), 934-943 (2006)
 16372191
 JOURNAL PUBMED
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 AUTHORS Zhang,X.-Y., Zhang,Y., Zhang,H.-J., Wang,S.-H. and Liu,L.
 TITLE Direct Submission
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DEFINITION      Human DNA sequence from clone RP11-131015 on chromosome 1 Containing
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                  (Hsp40) homolog subfamily B member 6 (DNABJ6) pseudogene and the 5'
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                  complete sequence.
ACCESSION      AL389925 AC026054
VERSION        AL389925.10 GI:11990046
KEYWORDS       HTG; DNABJ6; IL12RB2; IL23R.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE      Hall, R.
                Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
                Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
                Clone requests: clonerequest@sanger.ac.uk
                On or before Nov 12, 2004 this sequence version replaced
                GI:9309523, GI:11342817.
                The following abbreviations are used to associate primary accession
                numbers given in the feature table with their source databases:
                Eml; EMBL; Swi; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information
                on the WORMPEP database can be found at
                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                was generated from part of bacterial clone contigs of human
                chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                Group. Further information can be found at
                http://www.sanger.ac.uk/HGP/Chr1
                RP11-131015 is from the library RPCT-11.1 constructed by the group
                of Pieter de Jong. For further details see
                http://www.chori.org/bacpac/home.htm
                VECTOR: pBACe3.6
                ----- Genome Center
                Center: Wellcome Trust Sanger Institute
                Center code: SC
                Web site: http://www.sanger.ac.uk
                Contact: vegas@sanger.ac.uk
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                Draft Sequence Produced by Genome Sequencing Center, Washington
                University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                MO 63108, USA
                http://genome.wustl.edu/gsc/index.shtml
                This sequence was finished as follows unless otherwise noted: all
                regions were either double-stranded or sequenced with an alternate
                chemistry or covered by high quality data (i.e., phred quality >=
                30); an attempt was made to resolve all sequencing problems, such
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VERSION AX467352.1 GI:21900588
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1 Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
AUTHORS Hematopoietic receptors hprt and hprt2
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 DEFINITION
 Homo sapiens interleukin 23 receptor isoform 2 fl mRNA, partial
 cds, alternatively spliced.
 AY937251
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 1618)
 Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
 Wang,S.H. and Liu,L.
 Identification and expression analysis of alternatively spliced
 isoforms of human interleukin-23 receptor gene in normal lymphoid
 cells and selected tumor cells
 Immunogenetics 57 (12), 934-943 (2006)
 16372191

JOURNAL
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 Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
 Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
 location/Qualifiers

ORIGIN

Query Match 50.4%; Score 1440.2; DB 5; Length 1618;
 Best Local Similarity 90.7%; Pred. No. 0;
 Matches 1613; Conservative 1; Mismatches 4; Indels 161; Gaps 1;

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 Job time : 15919 secs

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Publication No. US20060106201A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masatatsu
APPLICANT: Yaguchi, Noriko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
FILE REFERENCE: 06501-105U81
CURRENT APPLICATION NUMBER: US/11/274, 375
PRIOR FILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: US/10/105, 930
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/JP00/06654
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: JP 2000-240397
PRIOR FILING DATE: 2000-08-03

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PRIOR FILING DATE: 1999-09-27
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1887)
US-11-274-375-9

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QY 1739 AGCAACAATATTTCTTGAAGATTTAAGCTCATATTAATCAAGAGAAATCAAGTTCT 1798
DB 1621 AGCAACAATATTTCTTGAAGATTTAAGCTCATATTAATCAAGAGAAATCAAGTTCT 1680
QY 1799 CTTGAATCAAAACCTGATGAGAGAGAAACCAACATGCTTTTGGAAAAATGATTCACC 1858
DB 1681 CTTGAATCAAAACCTGATGAGAGAGAGAAACCAACATGCTTTTGGAAAAATGATTCACC 1740
QY 1859 AGTGAATCTATTCAGAAAGACAGCCCTGCTTCTGATGAATTTTCTCTGTTGGGGATC 1918
DB 1741 AGTGAATCTATTCAGAAAGACAGCCCTGCTTCTGATGAATTTTCTCTGTTGGGGATC 1800
QY 1919 GTGAATGAGAGTTGCTCATCTATTAATCTTATTTTCCAAAAATTTTGGAAAGCCAC 1978
DB 1801 GTGAATGAGAGTTGCTCATCTATTAATCTTATTTTCCAAAAATTTTGGAAAGCCAC 1860
QY 1979 TTCAATGATTTTCACTTTGAAAGAGTGAAGTGTGTGCTCAAAATTCAA 2028
DB 1861 TTCAATGATTTTCACTTTGAAAGAGTGAAGTGTGTGCTCAAAATTCAA 1910

NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1301
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1284)
US-11-274-375-7

Query Match 43.3%; Score 1236.6; DB 8; Length 1301;
Best Local Similarity 99.8%; Pred. No. 3,6e-162;
Matches 1236; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 ATGATCAGTCACTATTCATGAGATGCAATATGAGCTTTCATCTTCACTCTTCACTG 178
DB 1 ATGATCAGTCACTATTCATGAGATGCAATATGAGCTTTCATCTTCACTCTTCACTG 60
QY 179 TGTGATGAGGATTTCAATATATACTGCTGGCCACATCTGGGTAGAACGAGCACA 238
DB 61 TGTGATGAGGATTTCAATATATACTGCTGGCCACATCTGGGTAGAACGAGCACA 120
QY 239 ATTTTAAAGTGGATGATATCTATATATTTGCAAGCACAATTAAAGATGCA 298
DB 121 ATTTTAAAGTGGATGATATCTATATATTTGCAAGCACAATTAAAGATGCA 180
QY 299 CCAAGAAATCTATTTTATATAAATGCGATCAAAAGAAATTTCAATCAAGAT 358
DB 181 CCAAGAAATCTATTTTATATAAATGCGATCAAAAGAAATTTCAATCAAGAT 240
QY 359 AATTAACCAACAGCTGGCTTGTATATAAATCTTCTGGAACACATGCTTATGTAC 418
DB 241 AATTAACCAACAGCTGGCTTGTATATAAATCTTCTGGAACACATGCTTATGTAC 300
QY 419 TGCATGCTGAATGTCCTCAACATTTTCAAGACACTGATATGTGAAAAAGACATTTCT 478
DB 301 TGCATGCTGAATGTCCTCAACATTTTCAAGACACTGATATGTGAAAAAGACATTTCT 360
QY 479 TCTGATATTCGCGCAATATTCCTGATGAAGTAACTGTCTATTAATATTCAGGC 538
DB 361 TCTGATATTCGCGCAATATTCCTGATGAAGTAACTGTCTATTAATATTCAGGC 420
QY 539 AATATGATCTGCACTGGAATGCTTGAAGTCACTCACTAATCAAAATATGCTGTA 598
DB 421 AATATGATCTGCACTGGAATGCTTGAAGTCACTCACTAATCAAAATATGCTGTA 480
QY 599 CATGTGAAGGTTAAGACAGAAAGACACAGTATCTCACTCAAGCTATATTAAC 658
DB 481 CATGTGAAGGTTAAGACAGAAAGACACAGTATCTCACTCAAGCTATATTAAC 540
QY 659 ATCTCACTGATTCATTTCAAGGTGCGAAGATCTTGTGGTCCAAAGCACAAC 718
DB 541 ATCTCACTGATTCATTTCAAGGTGCGAAGATCTTGTGGTCCAAAGCACAAC 600
QY 719 GCACTAAGGATGGAAGTCAAAACATGCAATTTCACTGATGATATAGGATACCT 778
DB 601 GCACTAAGGATGGAAGTCAAAACATGCAATTTCACTGATGATATAGGATACCT 650
QY 779 TCTGCAAGCCTGATTTCCAGGGCTGAGACTATTAATGCTACAGTGGCCAAAGCATAT 838
DB 661 TCTGCAAGCCTGATTTCCAGGGCTGAGACTATTAATGCTACAGTGGCCAAAGCATAT 720
QY 839 TATTTGGATGTCAAAACATTAAGATTTCTGCTGATTAATGATTAAGGCTTCA 898
DB 721 TATTTGGATGTCAAAACATTAAGATTTCTGCTGATTAATGATTAAGGCTTCA 780
QY 899 ACAAACCAACTGGAATGTTAAAGATTTGAACCAATTTTCAATGCAACAGTCA 958
DB 781 ACAAACCAACTGGAATGTTAAAGATTTGAACCAATTTTCAATGCAACAGTCA 840
QY 959 GAATTTACTTGAAGCCAAATTAAGTACGATTTCAAGTGAAGTCAAGAAACAGGC 1018

DB 841 GAATTTACTTGAAGCCAAACATTAAGTACGATTTCAAGTGAAGTCAAGAAACAGGC 900
QY 1019 AAAAGTACTGGAGCCTTGAGTTGACACCGTTTTCATTAACACCTGAAACAGTTCC 1078
DB 901 AAAAGTACTGGAGCCTTGAGTTGACACCGTTTTCATTAACACCTGAAACAGTTCC 960
QY 1079 CAGGTCAATCAAAACATTTCCAAATGACACATGAAATTTGGGTTAACAGTTGCTCC 1138
DB 961 CAGGTCAATCAAAACATTTCCAAATGACACATGAAATTTGGGTTAACAGTTGCTCC 1020
QY 1139 ATCTTCAAGGCACTTACTTCTGACAAACAGAGACATTTGACTTTTATGGGAATG 1198
DB 1021 ATCTTCAAGGCACTTACTTCTGACAAACAGAGACATTTGACTTTTATGGGAATG 1080
QY 1199 ATGCTTTTGGCTGATATGTCATATCTTCTTGAATGGGATTTTAACAGATATTC 1258
DB 1081 ATGCTTTTGGCTGATATGTCATATCTTCTTGAATGGGATTTTAACAGATATTC 1140
QY 1259 CGAAGTGGATTTAAAGAGATCTTATTTATACAAAGTGGCTTTATGAAGATAT 1318
DB 1141 CGAAGTGGATTTAAAGAGATCTTATTTATACAAAGTGGCTTTATGAAGATAT 1200
QY 1319 CCTAATATGAAAAACAGCAATGTTGAAAAATGCTACAG 1357
DB 1201 CCTAATATGAAAAACAGCAATGTTGAAAAATGCTACAG 1239

RESULT 5

US-11-274-375-1
Sequence 1, Application US/11274375
Publication No. US20060106201A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
FILE REFERENCE: 06501-105US1
CURRENT APPLICATION NUMBER: US/11/274,375
CURRENT FILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: US/10/105,930
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/JP00/06654
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: JP 2000-240397
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP 11-273358
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1784
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (98)...(1108)
US-11-274-375-1

Query Match 36.4%; Score 1039.2; DB 8; Length 1784;
Best Local Similarity 99.3%; Pred. No. 4.8e-135;
Matches 1041; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 28 CAGCGAACAAGGCTGAGCTGCTGTAAGGGAATATGCTTCAACAGGTTGAA 87
DB 7 CAGCGAACAAGGCTGAGCTGCTGTAAGGGAATATGCTTCAACAGGTTGAA 66
QY 88 AGAGGGAACAGCTTTTCTGCTTCCAGACATGAATCACTATTCATATGAGATGC 147
DB 67 AGAGGGAACAGCTTTTCTGCTTCCAGACATGAATCACTATTCATATGAGATGC 126
QY 148 AGTAATAGCCCTTTAATATCTTCAAGCTGCTGCTATGAGGAATTAATTAAC 207
DB 127 AGTAATAGCCCTTTAATATCTTCAAGCTGCTGCTATGAGGAATTAATTAAC 186

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QY 208 CTCGCGCACATCTGGGTAGAACCAAGCAATTTTAAAGATGGATATGATATCTCTAT 267
DB 187 CTCGCGCACATCTGGGTAGAACCAAGCAATTTTAAAGATGGATATGATATCTCTAT 246
QY 268 ATATTGCGAAGCGCAATTTAAAGATCTGCCAACAAGAACTTCAATTTTAAAGATGG 327
DB 247 ATATTGCGAAGCGCAATTTAAAGATCTGCCAACAAGAACTTCAATTTTAAAGATGG 306
QY 328 CATCAAGAAAGATTTCAATCAACAAGATTAATTAACAACAAGCTCGCTTGTATTA 387
DB 307 CATCAAGAAAGATTTCAATCAACAAGATTAATTAACAACAAGCTCGCTTGTATTA 366
QY 388 AATCTTCTGGAACCAATCTCTATATGATGCACTGCTGAATGTGCCAACAATTTCA 447
DB 367 AATCTTCTGGAACCAATCTCTATATGATGCACTGCTGAATGTGCCAACAATTTCA 426
QY 448 AGAGACATGATATGGAAGAAAGACATTTCTCTGGAATATCGCGCATATTTCTGATGA 507
DB 427 AGAGACATGATATGGAAGAAAGACATTTCTCTGGAATATCGCGCATATTTCTGATGA 486
QY 508 AGTAACCTGTGCTATTTATGATATTTCAAGCAACATGATCTGCACTGGAATCTGGA 567
DB 487 AGTAACCTGTGCTATTTATGATATTTCAAGCAACATGATCTGCACTGGAATCTGGA 546
QY 568 GCTCACCCTACATAGACCAAAATACGTGTACATGTGAAGATTTAGACACAGAAGA 627
DB 547 GCTCACCCTACATAGACCAAAATACGTGTACATGTGAAGATTTAGACACAGAAGA 606
QY 628 GCAACAGTATCTGACCTCAAGCTATATTAATCTCCAGATTTCAATTAAGATGGCA 687
DB 607 GCAACAGTATCTGACCTCAAGCTATATTAATCTCCAGATTTCAATTAAGATGGCA 666
QY 688 GAAGTCTTGTGGTCCCAAGCAAGCAAGCACTAGCATGGAAGATCAAAACA 747
DB 667 GAAGTCTTGTGGTCCCAAGCAAGCAAGCACTAGCATGGAAGATCAAAACA 726
QY 748 GCAATTCACCTGATATATGATATCTTCTGACAGCCGTCAATTTCCAGGCTGAG 807
DB 727 GCAATTCACCTGATATATGATATCTTCTGACAGCCGTCAATTTCCAGGCTGAG 786
QY 808 TATTAATGCTACAGTGGCCCAAGCAATTAATTTAGGATATGCAACAACATTTGAAA 867
DB 787 TATTAATGCTACAGTGGCCCAAGCAATTAATTTAGGATATGCAACAACATTTGAAA 846
QY 868 GATTTCCTGGAATGATATGATATCAAGCAAGCACTGGAATGTTAAAGATTT 927
DB 847 GATTTCCTGGAATGATATGATATCAAGCAAGCACTGGAATGTTAAAGATTT 906
QY 928 TGAACCAATTTTACATATGATGCAAGCAAGTCTTCTGAGCCAAACATTAAGTA 987
DB 907 TGAACCAATTTTACATATGATGCAAGCAAGTCTTCTGAGCCAAACATTAAGTA 966
QY 988 CGATATTTCAAGTATGATATGCAAGCAAGCAAGTCTTCTGAGCCAAACATTTAACC 1047
DB 967 CGATATTTCAAGTATGATATGCAAGCAAGCAAGTCTTCTGAGCCAAACATTTAACC 1026
QY 1048 GTTTTTCATTAACAACCTGAAACAGTT 1075
DB 1027 GTTTTTCATTAACAACCTGAAACAGTT 1054

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RESULT 6
US-10-539-228-682
; Sequence 682, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0052-101 (PPO23370.0003)
; CURRENT APPLICATION NUMBER: US/10/539,228
; PRIORITY FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/322,281

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; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682
; LENGTH: 36871
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-539-228-682

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Query Match      8.9%; Score 254; DB 6; Length 36871;
Best Local Similarity 77.8%; Pred. No. 2,7e-27;
Matches 305; Conservative 1; Mismatches 86; Indels 0; Gaps 0;

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QY 2468 AACAGCTCTCTATTTGTATGACAGAAAGGTAAATATGCAAAATACCTGTAGTAAATTA 2527
DB 32520 ACCACCCCTGATCTATATACAGAAATGAAATTAATTCATTTGTTTCAATGAAATTTG 32579
QY 2528 ATGCTGAAAATTTTCTTTTAAATTAATATCACTTAAGCCAGCGCTGTGCTATGCTTGT 2587
DB 32580 AACATTTTATCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 32639
QY 2588 AATCCAGCAGCTTGTGATGAGTGTGATGATCACTGAGTCAAGATTCAGATCC 2647
DB 32640 AATCCAGCAGCTTGTGATGAGTGTGATGATCACTGAGTCAAGATTCAGATTCAGATCC 32699
QY 2648 AGCCTGACCAATATGCTGAAACCTGTCTCTATTAATTAATTAATTAATTAATTAATTA 2707
DB 32700 AGCCTGCTCAACATGAGGAAACCCGCTCTCTATTAATTAATTAATTAATTAATTAATTA 32759
QY 2708 GTGGCAGGTGCTTTGATATCCCACTATCTGGAGAGCTGAGGAGGATTCATTAACC 2767
DB 32760 GTGGTGTGCGCTGTATATCCCACTGAGGAGGCTGAGGAGGATTCATTAACC 32819
QY 2768 AGGAAGCAGAGGTGCTGATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2827
DB 32820 TGGAGAGCAGAGGTGCTGATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 32879
QY 2828 GAGCAAACTCTGTCTGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2859
DB 32880 GAGCAAACTCTGTCTGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 32911

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RESULT 7
US-11-330-648-46/c
; Sequence 46, Application US/11330648
; Publication No. US20060211015A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 20366-042002
; CURRENT APPLICATION NUMBER: US/11/330,648
; PRIOR FILING DATE: 2006-01-12
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 44567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-330-648-46

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Query Match      8.7%; Score 248.6; DB 7; Length 44567;
Best Local Similarity 78.5%; Pred. No. 1.4e-26;
Matches 226; Conservative 1; Mismatches 80; Indels 0; Gaps 0;
QY 2483 TGTACAGAAAGGTAAATATATGCAAAATACCTGTGATTAATGCTGAAATTTTC 2542

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1	NAME/KEY:	exon
2	LOCATION:	12947..12958
3	OTHER INFORMATION:	exon 1
4	FEATURE:	
5	NAME/KEY:	exon
6	LOCATION:	13470..13526
7	OTHER INFORMATION:	exon 2
8	FEATURE:	
9	NAME/KEY:	exon
10	LOCATION:	13641..13752
11	OTHER INFORMATION:	exon 3
12	FEATURE:	
13	NAME/KEY:	exon
14	LOCATION:	14271..15968
15	OTHER INFORMATION:	exon 4
16	FEATURE:	
17	NAME/KEY:	misc feature
18	LOCATION:	15965..17969
19	OTHER INFORMATION:	3'regulatory region
20	FEATURE:	
21	NAME/KEY:	allele
22	LOCATION:	1239
23	OTHER INFORMATION:	20-828-311 : polymorphic base C or T
24	FEATURE:	
25	NAME/KEY:	allele
26	LOCATION:	12347
27	OTHER INFORMATION:	17-42-319 : polymorphic base C or T
28	FEATURE:	
29	NAME/KEY:	allele
30	LOCATION:	15241
31	OTHER INFORMATION:	17-41-250 : polymorphic base C or T
32	FEATURE:	
33	NAME/KEY:	allele
34	LOCATION:	42218
35	OTHER INFORMATION:	20-841-149 : polymorphic base A or G
36	FEATURE:	
37	NAME/KEY:	allele
38	LOCATION:	45442
39	OTHER INFORMATION:	20-842-115 : polymorphic base A or G
40	FEATURE:	
41	NAME/KEY:	allele
42	LOCATION:	77058
43	OTHER INFORMATION:	20-853-415 : polymorphic base C or T
44	FEATURE:	
45	NAME/KEY:	primer bind
46	LOCATION:	929..949
47	OTHER INFORMATION:	20-828.pu
48	FEATURE:	
49	NAME/KEY:	primer bind
50	LOCATION:	1357..1377
51	OTHER INFORMATION:	20-828.rp complement
52	FEATURE:	
53	NAME/KEY:	primer bind
54	LOCATION:	12029..12050
55	OTHER INFORMATION:	17-42.pu
56	FEATURE:	
57	NAME/KEY:	primer bind
58	LOCATION:	12581..12603
59	OTHER INFORMATION:	17-42.rp complement
60	FEATURE:	
61	NAME/KEY:	primer bind
62	LOCATION:	14992..15012
63	OTHER INFORMATION:	17-41.pu
64	FEATURE:	
65	NAME/KEY:	primer bind
66	LOCATION:	15460..15482
67	OTHER INFORMATION:	17-41.tp complement
68	FEATURE:	
69	NAME/KEY:	primer bind
70	LOCATION:	42070..42090
71	OTHER INFORMATION:	20-841.pu
72	FEATURE:	
73	NAME/KEY:	primer bind

LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
FEATURE:
NAME/KEY: primer bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
FEATURE:
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
FEATURE:
NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
FEATURE:
NAME/KEY: primer bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
FEATURE:
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
FEATURE:
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
FEATURE:
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
FEATURE:
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
FEATURE:
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
FEATURE:
NAME/KEY: misc binding
LOCATION: 12335..12359

OTHER INFORMATION: 17-42-319.probe
FEATURE:
NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
FEATURE:
NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
FEATURE:

Query Match 8.6%; Score 247; DB 7; Length 81001;
Best Local Similarity 86.6%; Pred.No.2.1e-26;
Matches 271; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

Qy 2547 AAAATGATCATTTAGGCGAGGCGTGGCTCATCTGTATCCACACCTTTGGTAG 2606
Db 65051 ATTAGGAATTTGTGTGGCCAGGTGCGATGGCTCAGCCCTGTATCCACACCTTTGGAG 64992
Qy 2607 GCTGAGTGTGATGATCAGCTGAGTCAAGAGTTGAGTCCAGCTGGCCATATGCTGA 2666
Db 64991 GCCAAGTGTGATGATCAGCTGAGTCAAGAGTTGAGTCCAGCTGGCCATATGCTGA 64932
Qy 2667 AACCGTCTCTACTAATAATTCAAAATTAAGCCGCGCANTGGTGGCAGGTCCTGTATATC 2726
Db 64931 AACCCGCTCTATTAATAATCAAAATTAAGCCGCGCANTGGTGGCAGGTCCTGTATATC 64872
Qy 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACAGAGAGGAGGTTGCAC 2786
Db 64871 CCAGCTACTCAGAGGCTGAGGCGAGAGATCACTTGAACCCGGAGAGGAGGTTGCAG 64812
Qy 2787 TGAGCTGAGATTTGGCCACTGCACTCCAGCTGGGCAACAGACAAACTGTGTGGA 2846
Db 64811 TGAGCTGAGATTTGGCCACTGCACTCCAGCTGGAGGAGCAAGAGCAGACTGTATCA 64752
Qy 2847 AAAAAAAAAAAAAA 2859
Db 64751 AAAAAAAAAAAA 64739

RESULT 9
US-10-669-920-341/C
Sequence 341, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
PRIOR FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 341
LENGTH: 438732
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (438732)
OTHER INFORMATION: n = A,T,C or G
US-10-669-920-341

Query Match 8.6%; Score 246.8; DB 6; Length 438732;

Best Local Similarity 88.7%; Pred. No. 1.6e-26;
Matches 266; Conservative 1; Mismatches 33; Indels 0; Gaps 0;

QY 2560 TAGCCAGCGGTGGTGGCTGATCTGTAATCCAGACCTTTGGTAGGCTGAGGTGGTG 2619
DB 404717 TAGGCCAGCGGTGGTGGCTGATCTGTAATCCAGACCTTTGGTAGGCTGAGGTGGTG 404658
QY 2620 GATCACCCTGAGGTGAGGAGTTGCGACCGCTGGCCAAAGGAGTGAACCCGCTCTGA 2679
DB 404657 GATCACCCTGAGGTGAGGAGTTGCGACCGCTGGCCAAAGGAGTGAACCCGCTCTGA 404598
QY 2680 CTAAATTAACAAATTAAGCCGCGCATGTGTGGCAGGTGCTTGTATCCAGCTACTTGGG 2739
DB 404597 CTAAATTAACAAATTAAGCTGTGGTGTGTGTGGGCGCTGTATCCAGCTACTGCGG 404538
QY 2740 AGGCTGAGCGAGAGAACTCTTGAACGAGAAAGCAGAGTTGCACTGAGCTGAGATTG 2799
DB 404537 AGGCTGAGCGAGAGAACTCTTGAACGAGAGTTGCACTGAGCTGAGATTG 404478
QY 2800 TGCCACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGGAATAAAAAAAAAA 2859
DB 404477 TGCCACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGGAATAAAAAAG 404418

RESULT 10

US-11-266-748A-292995

Sequence 292995, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

PRIOR FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: Patent version 3.3

SEQ ID NO 292995

LENGTH: 1000

TYPE: DNA

ORGANISM: Homo Sapiens

US-11-266-748A-292995

Query Match 8.6%; Score 245.4; DB 8; Length 1000;

Best Local Similarity 88.9%; Pred. No. 8.8e-26;
Matches 264; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 2563 GCCAGCGGTGGTGGCTGATCTGTAATCCAGACCTTTGGTAGGCTGAGGTGGTGAT 2622

DB 207 GCCAGCATGTGGCTCATGTTGTAATCTTGACATTTGGGAGGCTGAGGTGGTGAT 266

QY 2623 CACCTGAGTCAAGAGATTGAGTCCAGCGCTGGCCATATGCTGAACCCGTCTCTACTA 2682

DB 267 CATCTGAGTCAAGAGATTGAGTCCAGCGCTGGCCATATGAGTGAACCCGTCTCTACTA 326

QY 2683 AAATTAACAAATTAAGCCGCGCATGTGTGGCAGGTGCTTGTATCCAGCTACTTGGAGG 2742

DB 327 AAATTAACAAATTAAGCCGCGCATGTGTGGCAGGTGCTTGTATCCAGCTACTTGGAGG 386

QY 2743 CTGAGCGAGAGAACTCTTGAACGAGAAAGCAGAGTTGCACTGAGCTGAGATTGTGC 2802

DB 387 CTGAGCGAGAGAACTCTTGAACGAGAAAGCAGAGTTGCACTGAGCTGAGATTGTGC 446

QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGGAATAAAAAAAAAA 2859

DB 447 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGGAATAAAAAAAAAA 503

RESULT 11

US-11-266-748A-344424/C

Sequence 344424, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

PRIOR FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: Patent version 3.3

SEQ ID NO 344424

LENGTH: 1000

TYPE: DNA

ORGANISM: Homo Sapiens

US-11-266-748A-344424

Query Match 8.6%; Score 245.4; DB 8; Length 1000;

Best Local Similarity 88.9%; Pred. No. 8.8e-26;
Matches 264; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 2563 GCCAGCGGTGGTGGCTGATCTGTAATCCAGACCTTTGGTAGGCTGAGGTGGTGAT 2622

DB 794 GCCAGCATGTGGCTCATGTTGTAATCTTGACATTTGGGAGGCTGAGGTGGTGAT 735

QY 2623 CACCTGAGTCAAGAGATTGAGTCCAGCGCTGGCCATATGCTGAACCCGTCTCTACTA 2682

DB 734 CATCTGAGTCAAGAGATTGAGTCCAGCGCTGGCCATATGAGTGAACCCGTCTCTACTA 675

QY 2683 AAATTAACAAATTAAGCCGCGCATGTGTGGCAGGTGCTTGTATCCAGCTACTTGGAGG 2742

DB 674 AAATTAACAAATTAAGCCGCGCATGTGTGGCAGGTGCTTGTATCCAGCTACTTGGAGG 615

QY 2743 CTGAGGACGAGATCACTTTGAACACGAGAGGTTGCACTGAGCTGAGATTGTGC 2802
DB 614 CTGAGGACGAGATCACTTTGAACACGAGAGGTTGCACTGAGCTGAGATTGTGC 555
QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGAGAAAAA 2859
DB 554 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTCAAAAAA 498

RESULT 12

US-11-266-748A-404879
Sequence 404879, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harklin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 404879
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-404879

Query Match 8.6%; Score 245.4; DB 8; Length 1000;

Best Local Similarity 88.9%; Pred. No. 8.8e-26; Mismatches 32; Indels 0; Gaps 0;

Matches 264; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
QY 2563 GCCAGGCGTGTGGCTCATCTTGTATCCAGCACTTTGTAGGCTGAGGTGGTGGAT 2622
DB 207 GCCAGGCGTGTGGCTCATCTTGTATCCAGCACTTTGTAGGCTGAGGTGGTGGAT 266
QY 2623 CACTGAGGTCAAGAGTTTCAAGTCCAGCTGGCCCAATATCTGAAACCTGTCTTACTA 2682
DB 267 CACTGAGGTCAAGAGTTTCAAGTCCAGCTGGCCCAATATCTGAAACCTGTCTTACTA 326
QY 2683 AAATTCAAAAATTAAATGCGGCCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGAGG 2742
DB 327 AAATTCAAAAATTAAATGCGGCCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGAGG 386
QY 2743 CTGAGGACGAGATCACTTTGAACACGAGAGGTTGCACTGAGCTGAGATTGTGC 2802
DB 387 CTGAGGACGAGATCACTTTGAACACGAGAGGTTGCACTGAGCTGAGATTGTGC 446
QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGAGAAAAA 2859
DB 447 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTCAAAAAA 503

RESULT 13

US-11-266-748A-475925/c

Sequence 475925, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:

APPLICANT: Harklin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 475925
LENGTH: 1000
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-475925

Query Match 8.6%; Score 245.4; DB 8; Length 1000;

Best Local Similarity 88.9%; Pred. No. 8.8e-26; Mismatches 32; Indels 0; Gaps 0;

Matches 264; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
QY 2563 GCCAGGCGTGTGGCTCATCTTGTATCCAGCACTTTGTAGGCTGAGGTGGTGGAT 2622
DB 794 GCCAGGCGTGTGGCTCATCTTGTATCCAGCACTTTGTAGGCTGAGGTGGTGGAT 735
QY 2623 CACTGAGGTCAAGAGTTTCAAGTCCAGCTGGCCCAATATCTGAAACCTGTCTTACTA 2682
DB 734 CACTGAGGTCAAGAGTTTCAAGTCCAGCTGGCCCAATATCTGAAACCTGTCTTACTA 675
QY 2683 AAATTCAAAAATTAAATGCGGCCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGAGG 2742
DB 674 AAATTCAAAAATTAAATGCGGCCCATGTGTGAGGCTTGTAAATCCAGCTCACTTGGAGG 615
QY 2743 CTGAGGACGAGATCACTTTGAACACGAGAGGTTGCACTGAGCTGAGATTGTGC 2802
DB 614 CTGAGGACGAGATCACTTTGAACACGAGAGGTTGCACTGAGCTGAGATTGTGC 555
QY 2803 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTGAGAAAAA 2859
DB 554 CACTGCACTCCAGCTGGGCGAACAAGCAAACTCTGTCTCAAAAAA 498

RESULT 14

US-10-540-898-374
Sequence 374, Application US/10540898
Publication No. US20060166213A1
GENERAL INFORMATION:

APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: CHIR0056-101 (P023367.0003)
CURRENT APPLICATION NUMBER: US/10/540,898
CURRENT FILING DATE: 2005-06-27
PRIOR APPLICATION NUMBER: US 10/330,773
PRIOR FILING DATE: 2002-12-27

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; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 225587
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ... (225587)
; OTHER INFORMATION: n = A,T,C or G
US-10-540-898-374

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Query Match      8.6%; Score 244.8; DB 6; Length 225587;
Best Local Similarity 84.8%; Pred. No. 3.5e-26;
Matches 273; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

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QY 2537 ATTTTCCTTTAAATAGATCATTAGGCGGCGTGTGCTCATGCTTTGTAATCCAGC 2596
DB 139637 ATTTTAAATATAATATTTTATTTGGCCCGGCTGTGCTCATGCTTTGTAATCCAGC 139636
QY 2597 ACTTTGGTAGGCTGAGGTGGGTGATCAGCTGAGGTGAGGATTCGAGTCCAGCTGGCC 2656
DB 139697 ACTTTGAGAGGCTGAGGCGGATCAGCTGAGGTGAGGATTCGAGTCCAGCTGACC 139756
QY 2657 AATATGCTGAACCCCTGTCTCTCTAATAAATTACAAAAATTAGCCGATGTCAGGT 2716
DB 139757 AACATGGTGAACCCCTGTCTCTCTAATAAATTAGCCGATGTCAGGTGTCAT 139816
QY 2717 GCTTGTATCCAGCTACTTGGAGGCTGAGGAGGAAATCACTTGAACGAGAGGCA 2776
DB 139817 GCCTGTATCCAGCTACTTGGAGGCTGAGGAGGAAATCACTTGAACGAGAGGCA 139876
QY 2777 GAGGTGCACTGAGCTAGATTTGCACTGCACTCCAGCTGGGCAACAGAGCAAAAC 2836
DB 139877 GAGGTGCACTGAGCTAGATTTGCACTGCACTCCAGCTGGGCAACAGAGCAAAAC 139936
QY 2837 TCTGCTGAAAAAATAAATAA 2858
DB 139937 TCTGCTGAAAAAATAAATAA 139958

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RESULT 15
US-10-669-920-1403/c
; Sequence 1403, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1403
; LENGTH: 84105
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-669-920-1403

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Query Match      8.6%; Score 244.4; DB 6; Length 84105;
Best Local Similarity 85.0%; Pred. No. 4.8e-26;
Matches 272; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

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QY 2539 TTTCTTTAAATAGATCATTAGGCGGCGTGTGCTCATGCTTTGTAATCCAGC 2598
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QY 2599 TTTGTAAGGCTGAGGTGGGTGATCAGCTGAGGTGAGGATTCGAGTCCAGCTGGCCAA 2658
DB 69259 ATTGGAGGCGCGAGCGGCGGATCAGCTGAGGTGAGGATTCGAGTCCAGCTGGCCAA 69200
QY 2659 TATGCTGAACCCCTGTCTCTCTAATAAATAAATAAATTAGCCGATGTCAGGT 2718
DB 69199 CGTGTGAACCCCTGTCTCTCTAATAAATAAATAAATTAGCCGATGTCAGGTGTCAG 69140
QY 2719 TTTGAATCCAGCTACTTGGAGGCTGAGGAGGAAATCACTTGAACGAGAGGCA 2778
DB 69139 CTGTATCCAGATCTTGGAGGCTGAGGAGGAAATGCTTGAACGAGAGGCA 69080
QY 2779 GGTTCACCTGAGCTGAGATTTGCACTGCACTCCAGCTGGGCAACAGAGCAAAATC 2838
DB 69079 GGTTCACCTGAGCTGAGATTTGCACTGCACTCCAGCTGGGCAACAGAGCAAAATC 69020
QY 2839 TCTGCTGAAAAAATAAATAA 2858
DB 69019 TCTGCTGAAAAAATAAATAA 69000

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Job time : 573 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 14, 2006, 14:05:08 ; Search time 1043 Seconds
(without alignments)
6307.111 Million cell updates/sec

Title: US-10-667-289-2
Perfect score: 3326
Sequence: 1 MNXVITQMDAVIALYILFSM.....TYFPNLSHFNRISLKEK 629

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPRT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses02h
-USER=US1067289_@CEN_1_1_761_@rnat.13102006.11531.24352 -NCPU=6 -ICPU=3
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: geneseqn1980s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
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9: geneseqn2003bs: *
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11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *
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15: geneseqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3324	99.9	2859	6	AAK98257 Human DNA
2	3324	99.9	2859	13	AD873604 Human IL-
3	3324	99.9	2859	14	AA851089 Human DNA

4	3314	99.6	1890	14	ADV43392 Human pay
5	3314	99.6	1910	5	AA878822 Human hae
6	3314	99.6	2830	5	AD38773 Human hae
7	3292	99.0	2123	5	AA87820 Human hae
8	2952	88.8	1688	6	AD38774 Human hae
9	2747	82.6	1887	6	AAK98258 Human DNA
10	2280.5	68.6	1935	6	AD38777 Mouse hae
11	2192	65.9	1301	5	AA87821 Human hae
12	2175	65.4	1479	5	AA87819 Human hae
13	2039	61.3	1155	4	AA888149 Human DNA
14	2039	61.3	1155	10	ADCO7176 DNA encod
15	2039	61.3	1155	14	AD265011 DNA cyto
16	1868	56.2	1071	6	AD38775 Human hae
17	1747	52.5	1152	4	AA888150 Human DNA
18	1747	52.5	1152	10	ADCO7178 Human DNA
19	1747	52.5	1152	14	AD265013 Reverse t
20	1695	51.0	1784	5	AA87818 Human hae
21	266	8.6	360	5	AA87833 Human hae
22	256.5	7.7	2995	3	AAQ27656 gp130. 2/
23	256.5	7.7	2995	3	AA240299 Mouse gp1
24	256.5	7.7	2995	13	AD66595 Murine in
25	250	7.5	412	4	ABA46474 Human bre
26	225.5	6.8	3053	10	AD852498 Primary r
27	225.5	6.8	3053	13	AD66593 Rat inter
28	221	6.6	4023	6	ABQ78355 Nucleotid
29	216	6.5	2589	14	ADV43358 Human pay
30	216	6.5	3400	12	ADK90589 Human IL-
31	216	6.5	3400	12	ADM33786 Human IL-
32	216	6.5	4040	2	AA759731 Human int
33	216	6.5	4040	3	AA35207 Human ade
34	216	6.5	4040	3	AA721329 Human low
35	216	6.5	4040	6	ABK84394 Human CDN
36	216	6.5	4040	10	AD839703 Human int
37	216	6.5	4040	10	AD763394 Novel hum
38	216	6.5	4040	10	AB297023 Human pul
39	216	6.5	4040	11	ABD20872 Human pul
40	216	6.5	4040	12	ADO19579 Human PRO
41	216	6.5	4040	13	ADP54648 Human PRO
42	216	6.5	4040	14	ADY15767 DNA encod
43	216	6.5	4040	14	ADY19579 DNA encod
44	216	6.5	4040	14	ADY86629 Human int
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ALIGNMENTS

RESULT 1
ID AAK98257 standard; cDNA; 2859 BP.
XX AAK98257;
DT 28-MAY-2002 (first entry)
DE Human DNAX cytokine receptor subunit 5 (DCRS5) cDNA sequence.
XX Human; DNAX cytokine receptor subunit 5; DCRS5; IL30 receptor;
XX Immune response; DCRS5; p40/IL-130 ligand; cell physiology modulation;
XX cell development modulation; TH1-mediated disease; multiple sclerosis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX diabetes; psoriasis; sepsis; allogenic transplant; recipient;
XX TH2 response; tumour; viral growth; fungal growth; vaccine;
XX allergic response; gene; ss.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
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FT /product= "DCRS5 protein"
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FT /note= "Xaa= Gln or His"
FT /transl_except= (pos:563..545, aa:Xaa)

FT sig_peptide /note="Xaa= Arg or Gly"
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FT /*tag= b
FT 127
FT misc_feature /*tag= c
FT /note="If the base at this position is G (encoding Gln),
FT the base at position 563 is also G (encoding Gly). If the
FT base at this position is T (encoding His) the base at
FT position 563 is A (encoding Arg)"
FT 188. .2005
FT /*tag= d
FT /note="Mature DCRS5 protein"
FT 563
FT /*tag= e
FT /note="If the base at this position is G (encoding Gly),
FT the base at position 127 is also G (encoding Gln). If the
FT base at this position is A (encoding Arg) the base at
FT position 127 is T (encoding His)"
PN W0200185790-A2.
XX 15-NOV-2001.
XX 10-MAY-2001; 2001MO-US015057.
XX 10-MAY-2000; 2000US-0203426P.
XX (SCHE) SCHERING CORP.
XX Chirica M, Kastelein RA, Moore KW, Parham CL;
XX WPI; 2002-062238/08.
XX P-PSDB; AAO14008.
PT Novel DNA cytokine receptor subunit 5 polypeptide which is subunit of
PT receptor complex for p40/IL-830, useful for treating conditions
PT associated with abnormal expression or triggering of response to p40/IL-
PT B30 ligand.
XX
XX Claim 18; Page 9-12; 74pp; English.
XX
XX The present cDNA sequence encodes the human DNA cytokine receptor
XX subunit 5 (defined as DCRS5 or IL30 receptor) of the invention. DCRS5 is
XX a member of the class I branch of the cytokine receptor superfamily and
XX is closely related to the IL-6 receptor subunit gp130 and the IL-12R-Beta
XX -2 subunit. Cytokines are soluble molecules which play a critical role in
XX controlling the complex cellular interactions of the immune response. The
XX invention comprises novel receptors related to cytokine receptors
XX designated DNA cytokine receptor subunits (DCRS). Specifically the
XX invention comprises a subunit (DCRS5) for a receptor complex for the
XX p40/IL-B30 ligand. The DCRS5 proteins of the invention are useful for
XX treating diseases or disorders associated with abnormal expression or
XX abnormal triggering of response to the p40/IL-B30 ligand. The proteins of
XX the invention can be used to modulate the physiology or development of a
XX cell from a host which exhibits Th1-mediated disease; multiple sclerosis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX diabetes; psoriasis; sepsis; an allogeneic transplant recipient; chronic
XX Th2 response; tumor; viral or fungal growth; vaccine recipient; or an
XX allergic response
XX
XX Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;
SQ
SQ
Alignment Scores:
Pred. No.: 4, 9e-304 Length: 2859
Score: 3324.00 Matches: 629
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 6 Gaps: 0
US-10-667-289-2 (1-629) x AAK98257 (1-2859)
QY 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20

DB 119 ATGAATCAAGTCACTATTCAATGGAGTGAATAGCCCTTACATCTTCACCTGG 178
QY 21 CYNHIEGLVGIYIIEThraenIIeaenCysSerGIYHIEIETPrValGIUProAlaThr 40
DB 179 TGTCAATGAGAGATTCAATATATTAATCTCTGTGGCACAATCTGGGTATACACAGCAC 238
QY 41 IIEPheIYMeTGIYMeTAsnIIeSerIIeTYrCYeGlnAlaIIElyAsnCysGln 60
DB 239 ATTTTAATATGGGTATGATATATCTATATATTTGCAAGACGACATTTAAGAACTCCAA 298
QY 61 PROAlYLYLeuHISpHeTYrLYsaenGIYIIElyGIUaXGPhedInIIeThraGIIe 80
DB 299 CCAAGAAACCTCATTTTATATAAAATGGCATCAAGAAAGATTTCAATATCAAGAGATT 358
QY 81 AsnIYThThAlaArgLeuTPrTYrLYsaenPheLeuGIUProHISaIaSerMeTYr 100
DB 359 AATTAACAAACAGCTGGCTTGTTGTATTAACCTTCTGGAAACCAATGCTTATATGTC 418
QY 101 CysThraIAGIUCysProLYSHISpHeGlnIuThrLeuIIECysGIYLYsaPrlIeSer 120
DB 419 TGCACGTGTAATGTCCCAAAACATTTTCAAGAGACACTGATATGTGAAAACATTTCT 478
QY 121 SerGIYTYrProProlaPrlIeProaPrlValIIEThCysValIIEtyrGIUtyrSerGIY 140
DB 479 TCTGATATCCGCCAGATATTCCTGATYGAAGAACTGTGTCAATTATATATTCAGGC 538
QY 141 AsnMeTThCysThrThraenIIa**LYsLeuThTYrIIEspThrLYsTYrValI 160
DB 539 AACATACCTTGACCTCGAATGCTRGAAAGCTCACTCAATAGACAAATAATCGTGTA 598
QY 161 HIEValIYseSerIeugIuThrgIuGlnIuGlnIuThrLeuThseSerTYrIIEaen 180
DB 599 CATGTAAAGATTATAGACAGAAAGAGCAACATATCTCACTCAAGCATATATTAAC 658
QY 181 IIESerThAspSerIeugInGIYLYsLYsTYrLeuValITPrAlaGlnAlaIaen 200
DB 659 ATCTCCAGTATCATTAAGGTGCAAGAGTACTCTGTGTGGGTCCAAAGGCAAAC 718
QY 201 ALIEuGIYMeTGIUSeSerLYsGlnIeugInIIeHIEleuAspPrlIeValIIEPro 220
DB 719 GCACGTAGCATGAAAGTCAAAACATGCAAAATTCACCTGATATATAGATACCT 778
QY 221 SerAlaIeValIIESerIaGlnIuThrIIEaenIIeThraIProIyThrIIEIIE 240
DB 779 TCTGACGCGTCAATTTCCAGGCTGAGCATATTAAGTCAAGTCCCAAGACCAATAAT 838
QY 241 TYrTrpAspSerGlnThrThrIIEGIYLYsValIIEserCYeGIUMeTArgTYrLYsaIaThr 260
DB 839 TATTTGGATATGTCAAACAAATTTGAAGGTTCTGTGAAATGAGATCAAGGCTTAC 898
QY 261 ThraenGIThThraenValIYsGIUPheAsPrlThraPheThTYrValIIEGlnIeSer 280
DB 899 ACNAAACCAACTTGGAAATGTTAAAGATTTGACACCAATTTTACATATGTGCAACGTCA 958
QY 281 GIUPheTYrLeuGIUProAsnIIeLYsTYrValIIEGlnValIaArgCYeGlnIuThrgIY 300
DB 959 GAATTCACCTTGAAGCCAAACATTAAGTACGTATTTCAAGTGAAGTCAAGAAAGAGGC 1018
QY 301 LYsaIArgTYrTrpGlnProTrpSerSerProPhePheHISpHeThProGIUThrValIPro 320
DB 1019 AAAAGTACTGGAGCGCTTGAGATTCAACGTTTTCATATAAACACCTGAAACAGTTCCC 1078
QY 321 GlnValThSerLYsaIaPheGlnHISaPrlThThraPnSerGIYLeuThrValIaIeSer 340
DB 1079 CAGGTACATCAAAACATTTCCAACTGACACATGGAATTTCTGGGTAAACAGTTGCTTC 1138
QY 341 IIESerThGIYHISLeuThSerAspAsnArgGIYAsPrlIEGIYLeuIeugIYMeT 360
DB 1139 ATCTTACAGGGACCTTACTCTGACAAACAGAGAGACATTTGAACTTTATTTGGAAATG 1198
QY 361 IIEValPheAlaValMeTLeuSerIIEleuSerIeIIeGIYIIEPheAsnArgSerPhe 380

Db	1199	ATGCGCTTGCGTATATGTCATATTCCTTCTTGATTGGGATATTAAACAGATCATTC	1258
Qy	381	Argthrnglyllelvsargargllleleuleuleullepolyetfpleurygluaspille	400
Db	1259	CGAAGCTGGGAATTTAAAGAAAGGATCTTATTGTAAATACAAAGTGCTTTATGAAAGATATT	1318
Qy	401	ProasmetlvsAsnSerAsnValValylsMetLeuGlnGluAsnSerGluMetAsn	420
Db	1319	CTTATATGAAAACGCAATGTGTGTGAAATGCTACAGGAAATATGGAAGCTTATGAT	1378
Qy	421	AsnAsnSerSerGluGlnValleuTyValAspProwetllethGluillelvsGluile	440
Db	1379	AATATATTCAGTGAGCAGAGCTCCTATATTTGATGCCAGATTACAGATATAAGAAATC	1438
Qy	441	PheilleProGluHselysProThrAspTyrylsylsGluAsnThrGlyProleuGluThr	460
Db	1439	TTTCATCCAGAAACACAAAGCTTACAGACTACAAAGAGGAATATACAGAGCCCTGGAGACA	1498
Qy	461	ArgAspTyProGluInAsnSerLeuPheAsnThrThrValValTyrlleProAspLeu	480
Db	1499	AGAGACTACCCGCAAAATCCGCTATTCAGACAAATACAGTTGATATATTCCTGATCTC	1558
Qy	481	AsnThrGlyTyrylvsProGlnlleseAsnPheLeuProGluGlySerHisleuSerAsn	500
Db	1559	AACACTGGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAGGAGCACTCAGCAT	1618
Qy	501	AsnAsnGluillethSerLeuThrleuLysProValAspSerLeuAspSerGlyAsn	520
Db	1619	AATATATGAAATTAATCTCTTAACTTAACCTTAACCAACAGTTGATTCCTTAGACTCAGGAAT	1678
Qy	521	AsnProAspGluGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu	540
Db	1679	AATCCCAAGGTACAAAGACATCCATAATTTCTGTTTCTGTTTCAAGTGAATTCACCTA	1738
Qy	541	SerAsnThrillePheLeuGluLeuSerLeuileuAsnGlnGluCysSerSer	560
Db	1739	AGCAACACAAATATTTCTTGAGAAATTAGCCCTCATATTAATCAAGAGAAATGACGTTCT	1798
Qy	561	ProAspilleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro	580
Db	1799	CCTGACATACAAAATCTCAGTAGAGAGGAAACCAACAGCTTTTGGAATAAGATTCAACC	1858
Qy	581	SerGluThrilleProGluGlnThrleuLeuProAspGluPheValSerCysLeuGlylle	600
Db	1859	AGTAAACTATTCAGAAACAGACCCCTGCTCTGATGAATTTGCTCCTGTTGGGATTC	1918
Qy	601	ValAsnGluGluLeuProSerilleAsnThrTyrrPheProGlnAsnilleLeuGluSerHis	620
Db	1919	GTCGATGAGGAGTTCACATTAATTAATCTTAATTTTCCACAAAATATTTTGAAAGCCAC	1978
Qy	621	PheAsnArgilleSerLeuLeuGluLys	629
Db	1979	TTCAATAGGATTTCACTTTGGAAAAG	2005
RESULT 2			
ADST73604	ID	ADST73604	standard; cDNA; 2859 BP.
AC	ADST73604;		
XX	16-DEC-2004	(first entry)	
DT			
XX			
DE			
XX	Human IL-23R coding sequence.		
KM	ss; gene; human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour;		
KM	growth; agonist; antagonist; receptor; cancer; antigen-binding site;		
KM	antibody; extracellular region; antisense nucleic acid;		
KM	small interference RNA; siRNA; polyclonal; monoclonal; humanized; Fab;		
KM	Fv; Fab/2; peptide mimetic; colon; ovarian; breast; melanoma; cachexia;		
KM	anorexia; angiogenesis; gastrointestinal tract; respiratory tract;		
KM	reproductive system; endocrine system.		
XX			
XX	Homo sapiens		
DS			

XX	Key	Location/Qualifiers
FH	CDS	119..2008
FT		/*tag= b
FT	sig_peptide	/product= "IL-23r"
FT		119..187
FT	mat_peptide	/*tag= a
FT		188..2005
FT		/*tag= c
PV		MO2004081190-A2.
PD	23-SEP-2004.	
PF	09-MAR-2004; 2004WO-US007198.	
PR	10-MAR-2003; 2003US-0453672P.	
PA	(SCHE) SCHERING CORP.	
PX	Otc M, Mcclanahan TK;	
PX	WPI: 2004-668951/65.	
DR	P-PSDB; ADS73605.	
XX		Modulating tumor growth, useful for treating a subject suffering from cancer or tumor, comprises contacting a tumor cell with an agonist or antagonist of IL-23.
PT		
PT		
PS	Claim 4; SEQ ID NO 5; 57pp; English.	
XX		This sequence encodes human interleukin 23 receptor (IL-23R). The method of the invention for modulating tumor growth comprises contacting a tumor cell with an agonist or antagonist of IL-23. The agonist or antagonist is a binding composition which specifically binds the IL-23 p19 subunit (IL-23p19) or the IL-23R protein. The identified agonist or antagonist may be used for diagnosing or treating a subject suffering from a cancer or tumor. The binding composition comprises an antigen-binding site of the antibody, an extracellular region of IL-23R, a small molecule, an antisense nucleic acid or small interference RNA (siRNA), or a detectable label. The binding composition comprises a polyclonal antibody, a monoclonal antibody, a humanized antibody or its fragment, a Fab, Fv, F(ab') ₂ fragment, or a peptide mimetic of an antibody. The tumour cell is a colon, ovarian or breast cancer cell, or melanoma cell. In the treatment method, the antagonist of IL-23 inhibits growth of cancer or tumour, cachexia, anorexia or angiogenesis. The cancer or tumour is of the gastrointestinal tract, respiratory tract, reproductive system or endocrine system. In diagnosing cancer or tumour, the binding composition comprises a nucleic acid probe or primer that specifically binds or hybridizes to human or mouse IL-23p19 cDNA sequences, or the human IL-23r sequence.
XX		
SO	Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;	
Alignment Scores:		
Pred. No.:	4..9e-304	Length: 2859
Score:	3324..00	Matches: 629
Percent Similarity:	100.0%	Conserves: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	99.9%	Indels: 0
DB:	13	Gaps: 0
US-10-667-289-2 (1-629) X ADS73604 (1-2859)		
OY	1 MetAsn***ValThrIleGlnTrpAspAlaValIlealaLeuTyrlleleupheserTrrp 20	
Dd	119 ATAAATCAAGCTCATTCATCAATGGAGATCAGAAATAGCCCTTTACATCTTCAGCTGG 178	
OY	21 CYSHISGLIGLIVILETHRAAILLEASNCYSSEERGIYHSIILETSPVALGISLPFOALATHr 40	
Dd	179 TGTCATGGAGGAATTTCAAATTTAATACGTGCCTCGGCCAACATCTGGTGAGAACAAGCCACA 238	
OY	41 IIPheLYMeGcLYMeCAsnIlleSeerITyrcYsgInlaLaIleLybaNcYseGln 60	

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Db      |||
239  ATTTTAAGATGGGTGATGATCTCTATATATGCGCAACAGCAATTAAAGAACTGCCAA 298
Qy      |||
61  ProArgLeuLeuHisPheTyrLysAsnGlyIleValGluLysPheGlnIleThrArgIle 80
Db      |||
299  CCAAGGAACTCTCATTTTATTAATAATGCAATCAAGAAAGATTTCAATATCAAGAAATT 358
Qy      |||
81  AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuLysProHisIleSerMetTyr 100
Db      |||
359  AATTAACAACACAGCTGGCTTTGGTATATAAAACCTTCTGGAACCACTGCTTATATGTA 418
Qy      |||
101  CysThrAlaGluCysProLysHisPheGlnIleThrLeuIleCysGlyLysAspIleSer 120
Db      |||
419  TGCACCTGCTGAATGTCCTCAAAACATTTTCAAGAGACACTGATATGTGAAAAAGCATTTCT 478
Qy      |||
121  SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
Db      |||
479  TCTGGATATCCGGCCAGATATTTCTGATGAAGTAACTGTGCTATTATGAAATTTTCAGGC 538
Qy      |||
141  AsnMetThrCysThrTyrPheAsnAla**LysLeuThrTyrIleAspThrLysTyrValVal 160
Db      |||
539  AACATGACTTGCACTGGAAATGCTGGAGACTCACTCAATPAGCACAAAATACGTGTA 598
Qy      |||
161  HisValLysSerLeuGluLysGluGluGluGlnIleTyrLeuThrSerSerTyrIleAsn 180
Db      |||
599  CATGTGAAGAGTTTGAAGACAGAAAGAACCAAGATCTCACTCAACCTATATTAAAC 658
Qy      |||
181  IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGlnAlaIleAsn 200
Db      |||
659  ATCTCCACTGATTCATTAACAAGGTGGCAAGAGTACTTGTTGGTTCACCAAGCAAAAC 718
Qy      |||
201  AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisIleLysAspAspIleValIlePro 220
Db      |||
719  GCATGACGATGAGAAAGATCAAAACCACTCAATTCACCTGATGATATATGATGATCCT 778
Qy      |||
221  SerAlaAlaValIleSerArgIleGluThrIleAsnAlaThrValProLysThrIleIle 240
Db      |||
779  TCTGCACCCGCTCATTTCCAGGGCTGAGACTATTAATCTACAGGCCCAAGACCATATT 838
Qy      |||
241  TyrThrAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
Db      |||
839  TATTGGATATGTCAAACAACAATTAAGAAAGTTTCCGTGTAATGATACAAAGCTTACA 898
Qy      |||
261  ThrAsnGlnThrTyrPheAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
Db      |||
899  ACAAAACCAACTTGATGATGTTAAAGATTTGACCAATTTTACATATGAGCAACACTCA 958
Qy      |||
281  GluPheTyrLeuGluLysProAsnIleLysTyrValPheGlnValArgCysGlnIleThrGly 300
Db      |||
959  GAATTTCTACTTGAGCCAAACATTAAGTACGTATTTCAAGTGAAGATGTCAAGAAACAGGC 1018
Qy      |||
301  LysArgTyrTyrGlnProIleProSerSerProPhePheHisIleThrProGluThrValPro 320
Db      |||
1019  AAAAGGTACTGGCCCTTGAGTTCACTGTTTTCATTAATAACCTGAAACAGTTCC 1078
Qy      |||
321  GlnValThrSerLysAlaPheGlnHisAspThrTyrPheAsnSerGlyLeuThrValAlaSer 340
Db      |||
1079  CAGGTCACTCAATAAAGATTCACACATGACACATGGAATTCGTGGCTTAAAGTTGCTTC 1138
Qy      |||
341  IleSerThrGlyHisLeuThrSerAspAsnArgIleAspIleGlyLysLeuLeuGlyMet 360
Db      |||
1139  ATCTCTACAGGGCACCTTACTTCTGACCAACAGAGAACATGTGACCTTTATTGGGAATG 1198
Qy      |||
361  IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db      |||
1199  ATGCTCTTGTCTGTATGTTGTCATATCTTCTTGTATGGGAATATTTAACAGATCAATTC 1258
Qy      |||
381  ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrPleuTyrGluAspIle 400
Db      |||
1259  CGAACTGGGATTAAAGAAGATCTTATTTGTTATACCAAGTGGCTTTATGAAGATATT 1318
Qy      |||
401  ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420

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Db      |||
1319  CCTAATATGAAAAACGCAATGTTGTGAAAAATGCTACAGAAAAATAGTGAATTTATGAAT 1378
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421  AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440
Db      |||
1379  AATTAATTCAGTAGAGAGAGGTCCCTATATGTTGATCCCATGATTAACAGATTAATAAAGAAATC 1438
Qy      |||
441  PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
Db      |||
1439  TTCATCCCAAGAACACAAAGCTACAGACTACAGAAAGAAATACAGAGACCCCTCGAGAGCA 1498
Qy      |||
461  ArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
Db      |||
1499  AGAGACTACCCGCAAACTCGCTATTGACATACTACAGTTGTATATTTCTGTAATCTC 1558
Qy      |||
481  AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisIleSerAsn 500
Db      |||
1559  AACACTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGGAAGCCATCTCAAGCAAT 1618
Qy      |||
501  AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db      |||
1619  AATTAATGAATTAATCTTCTTAACACTTAACCACTTAAGATTCCTTACACTCAAGAAAT 1678
Qy      |||
521  AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db      |||
1679  AATCCAGGTACAAAGACATCTTAATTTGCTTTTCTGTTTCAAGTGTGAATTCACATA 1738
Qy      |||
541  SerAsnThrIlePheLeuGlyLysLeuSerLeuIleLeuAsnGlnGlyLysCysSerSer 560
Db      |||
1739  AGCAACACATATTTCTTGAGAAATTAACTTCAATTAATCAAGAGAAATGCAAGTTCT 1798
Qy      |||
561  ProAspIleGlnAsnSerValGluGluGluLysThrMetLeuLeuGluAsnAspSerPro 580
Db      |||
1799  CCTGACATACAAACCTCACTAGAGAGAGAAACCAACATCTTTGGAAAAATGATTAACCC 1858
Qy      |||
581  SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db      |||
1859  AGTGAACATATTCACAAACAGACCTGCTTCTGATGAATTTGTCCTGCTTTGGGGAATC 1918
Qy      |||
601  ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnSerHis 620
Db      |||
1919  GTGAATGAGAGTTGCATCTATTAATACCTTATTTCCAAAAAATTTTGGAAACCCAC 1978
Qy      |||
621  PheAsnArgIleSerLeuLeuGlyLys 629
Db      |||
1979  TTCAATATGATTTTCACCTTGTGAAAAAG 2005

RESULT 3
ID      AEA51089
ID      AEA51089 standard; DNA; 2859 BP.
XX      AEA51089;
AC      AEA51089;
XX      11-AUG-2005 (first entry)
DT      XX
XX      Human DNAX cytokine receptor subunit 5 (DCRSS) DNA.
DE      XX
XX      Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder;
XX      inflammation; respiratory disease; allergy; antiallergic;
XX      chronic obstructive pulmonary disease; respiratory-gen.;
XX      pulmonary fibrosis; anti-inflammatory; pneumonia; infection;
XX      cytokine receptor family; gene; ds.
OS      Homo sapiens.
XX      XX
FH      Key      Location/Qualifiers
FT      sig_peptide      1..187
FT      CDS      /*tag= a
FT      /*tag= b      119..2008
FT      /*product= "Human DNAX cytokine receptor subunit 5 (DCRSS)
FT      protein"
FT      /*transl_except= (pos:125..137, aa: Xaa)
FT      /*note= "Xaa corresponds to Gln or His"

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FT      /transl_except= (pos:563..565, aa: Xaa)
FT      /note= "Xaa corresponds to Gly or Arg"
FT      mat_peptide 188..2005
FT      /*tag= c
FT      /product= "Mature human DNAX cytokine receptor subunit 5
FT      (DCRS5) protein"
XX      WO2005052157-A1.
XX      09-JUN-2005.
XX      18-NOV-2004; 2004MO-US038886.
XX      21-NOV-2003; 2003US-00720026.
XX      (SCHE ) SCHERING CORP.
XX      Chirica M, Kaetelein RA, Moore KW, Parham CL;
XX      WPI; 2005-41800/42.
XX      P-PDB; AEA51090.
PT      Use of an agonist or antagonist of DNAX cytokine receptor subunit 5
PT      (DCRS5) or of p19 for treating a human subject experiencing a
PT      physiological disorder such as allergy or chronic obstructive pulmonary
PT      disorder (COPD).
XX      Claim 1; SEQ ID NO 1; 89pp; English.
XX      The present invention relates to a method of treating a human subject
XX      experiencing a physiological disorder. The method involves administering
XX      an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5, also
XX      known as IL-23r) or of p19, where the disorder comprises asthma or
XX      allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial
XX      lung disorder. The invention is useful for treating interstitial lung
XX      disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and
XX      hypersensitivity pneumonitis. The present sequence is the human DCRS5
XX      DNA.
XX      SQ      Sequence 2859 BP; 929 A; 575 C; 560 G; 791 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:      4.9e-304      Length:      2859
Score:          3324.00      Matches:      629
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:      99.9%      Indels:      0
DB:              14      Gaps:      0

US-10-667-289-2 (1-629) x AEA51089 (1-2859)
QY      1 MetAan**ValThrIleGlnTTPAPAlaValIleAlaLeuTYrIleLeuPheSerTIP 20
DB      119 ATGAAATCAKGTCACTATTCAATGGATGAGATGAGATATACCCCTTACATACCTCTCAGCTGG 178
QY      21 CyHhIeGlyGlyIleThrAenIleAenCySerGlyVhIleTTPVAlGluProAlaThr 40
DB      179 TGCATGAGAGAAATTACAAATATTAACCTGCTGGCCACATCTGGGTAGAACAGCCACA 238
QY      41 IlAPheIleWetGlyMeCaenIleSerIleTYrCySgIlnAlaIleIleIleYAsnCySgIln 60
DB      239 ATTTTAAAGTGGTATGATATCTCTATATATTGCCAGACAGAAATTGAAGACTGCA 298
QY      61 ProArGlyLeuHhIeSHeTYrLYVAsnGlyIleIleSgIlnArGheGlnIleThrArgIle 80
DB      299 CCAAGGAAACTTCATTTTATAAAATATGCAATCAAAAGATTTCAAATCACAAGGATT 358
QY      81 AsnLysThrThrIlaaGleuThrTYrLYVAsnPhelengIuprOHsAlaSerMetTYr 100
DB      359 AATTAACAAACAGCTGGCTTGGATTAATAAATCTTCGAAACCAATGCTTCTATATAC 418
QY      101 CyethrIlaGluCyProLYSHIePhelGlnIleThrLeuIleCySgIlyIleAspIleSer 120

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DB      419 TGCATGCTGATGTCTCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGCATTTCT 478
QY      121 SerGlyTYrProProAspIleProAspGluValThrCyValIleTYrGlyTYrSerGly 140
DB      479 TCTGATATCCCGCAATATTCCTGATGAGATTAACCTGTGTCTATTATGAAATTTACGGC 538
QY      141 AsnMetThrCySHeThrTPAenAla***LYleuThrTYrIleAspThrLYVAlVal 160
DB      539 AACATGACTTGCACCTCGAATGCTRGAAGCTCACCACATACATACAAATAATCGGTGA 598
QY      161 HsValLYSerIleuGluThrGluGluGluGluGluGluGluGluGluGluGluGluGlu 180
DB      599 CATGTAAAGATTTAAGACAGAGAAAGCAACAGATATCTCACTCAAGCTATATTAAC 658
QY      181 IlSerThrAspSerLeuGlnGlyIleLYSlyTYrLeuValTYrValGlnAlaIleAsn 200
DB      659 ATCTCACTGATTCATTACAGGTGCAAGAAATGACTTGTTGGGTCCAGAGCAAC 718
QY      201 AlaLeuGlyMeGluGluSerLYSlyGluLeuGlnIleHsIleuAspAspIleValIlePro 220
DB      719 GCACTAGCATGGAAAGTCAAAACACTGCAAAATTCACCTGGATGATATAGTATACCT 778
QY      221 SerAlaAlaValIleSerArgIleGluThrIleAsnAlaThrValProLYSThrIleIle 240
DB      779 TCTGACCGCTCATTTCCAGGCTGAGACTATATAATGCTACAGTCCCAAGACCATTAAT 838
QY      241 TYrTPAspSerGlnThrThrIleGluLYVAlSerCySgIlnWetArgTYrLYSAlaThr 260
DB      839 TATTTGGATATGTAAACAAACATTTGAAGAGTTTCTGTGAATATGATCAAGGCTACA 898
QY      261 ThrAsnGlnThrTPAsnValLYSgIlnPheAspThrAsnPhelThrTYrValGlnGlnSer 280
DB      899 ACAACCAAACTTGAAATGTAAAGATTGAACCAATTTTCAATATGCAACAGTCA 958
QY      281 GluPheTYrLeuGluProAsnIleLYSlyTYrValPhelGlnValArgCYSGlnGluThrGly 300
DB      959 GAATTTACTTGGAGCAACATTAAGTACATTTCAAGTGAAGTCAAGAAACAGGC 1018
QY      301 LYsArgTYrTPGlnProTPSerSerProPheHhIeLYSThrProGluThrValPro 320
DB      1019 AAAAGTACTGGCAGCGCTTGAGCTTCAACGTTTTCATTAACACCTGAAACAGTTCCC 1078
QY      321 GlnValIleSerLYSAlaPheGlnHhIeAspThrTPAsnSerGlyLeuThrValAlaSer 340
DB      1079 CAGTCACATCAAAACATTTCAACATGACACATGGAATTCGCGGCTTAACAGTTGCTTC 1138
QY      341 IlSerThrGlyHhIeLeuThrSerAspAsnArgLYAspIleGlyLeuLeuLeuGlyMe 360
DB      1139 ATCTTACAGGGCACTTACTTGTGACAAACAGAGACATTTGACCTTTATTTGGGATG 1198
QY      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
DB      1199 ATGCTCTTGCTATATGTTGTAATCTTCTTGTGAGATTTTAACAAGTATTC 1258
QY      381 ArgThrGlyIleLYSArgArgIleLeuLeuLeuIleProLYSThrPleuTYrGluAspIle 400
DB      1259 CGAATCGGATTAAGAAGAGATCTTATGTTAATCAAAAGTGGCTTATGAAGATAT 1318
QY      401 ProAsnMetLYSAsnSerAsnValIleLYSMeLeuGlnIleuAsnSerGluLeuMetAsn 420
DB      1319 CTTAATATGAAAAACGCAATGTTGTGAATAATCTCAGGAAAAATGTGAACTTAATCAAT 1378
QY      421 AsnAsnSerSerGluGlnValIleuTYrValAspProMetIleThrGluIleLYSgIle 440
DB      1379 AATTAATTCAGTAGAGGTCTTATATGTAATCCATGATTAACAGATTAAGAAATC 1438
QY      441 PheIleProGluHhIeLYSProThrAspTYrLYSgIlnuAsnThrGlyProLeuGluThr 460
DB      1439 TTATCCCAAGAACACAAAGCTTACAGACTACAAAGAGAAATACAGAGACCCCTGAGACA 1498
QY      461 ArgAspTYrProGlnAsnSerLeuPheAspAsnThrThrValValTYrIleProAspLeu 480
DB      1499 AGAGACTACCCGAAAACCTGCTATTTGACAAATACATACAGTTGTATATATCTCTGATCTC 1558

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QY 481 AenThrGlyTyrIysProGlnIleSerAenPheLeuProGlnIleSerHisIleuSerAen 500
 Db 1559 AACACTGATATTAACCCCAATTTCTGCTGAGGAGAACCATCTCAGCAAT 1618
 QY 501 AenAenGlnIlePheSerLeuThrLeuProProValAenPheSerLeuAenSerGlyAen 520
 Db 1619 AATTAAGAAATTAATCTTCTTAACCTTAACCAACCACTTAATCTTAAGCTCAGGAAT 1678
 QY 521 AenProAenGlnIlePheSerAenPheAenPheSerAenSerAenSerLeu 540
 Db 1679 AATCCAGGATTAACAAAGCATCTTAATTTGCTTTCTGTTCAATGGAATTCATA 1738
 QY 541 SerAenThrIlePheLeuGlnIleuSerLeuIleuAenGlnIleuGlnIleuSerSer 560
 Db 1739 AGCAACACATATTTCTTGAAGAAATTAAGCTCATATTAATCAAGAGAAATCAGATTCT 1798
 QY 561 ProAenPheIleGlnAenSerValGlnIleuGlnIleuThrTherLeuGlnIleuAenPhePro 580
 Db 1799 CCGACATACAAACCTCAGTAGAGAGAAACCAACCTGCTTTGAAATGATCAACC 1858
 QY 581 SerGlnThrIleProGlnIleuThrLeuProAenPheValSerCysLeuGlyIle 600
 Db 1859 AGTGAACATTTCTCAGAACAGACCCCTGCTTCTGATGAATTTGCTCTCTTTGGGATC 1918
 QY 601 ValAenGlnIleuProSerIleAenThrTyrPheProGlnAenIleuGlnIleuSerHis 620
 Db 1919 GTCAATGAGAGTGGCATCTATTAATTAATTTTCCAAATATTTTGAAGACCAAC 1978
 QY 621 PheAenArgIleSerLeuGlnIleu 629
 Db 1979 TTCAATAGATTTCACTTGAAGAAAG 2005

RESULT 4

ADV43392 standard; cDNA; 1890 BP.

ADV43392;

10-MAR-2005 (first entry)

Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1020.

microarray; psychoneuroendocrinimmune; chronic fatigue;
 non-insulin dependent diabetes; allergy; immune disorder; inflammation;
 cancer; neoplasm; infection; expressed sequence tag; ss.

Homo sapiens.

MO2004108899-A2.

16-DEC-2004.

04-JUN-2004; 2004MO-US017686.

04-JUN-2003; 2003US-0475915P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Nicholson A, Vernon SD;

WPI; 2005-031682/03.

New microarray comprising probes for genes involved in
 psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
 condition associated with PNI activity, e.g., inflammatory or infectious
 diseases.

Claim 1; SEQ ID NO 1020; 254bp; English.

The invention relates to a new microarray which comprises probes for
 genes involved in psychoneuroendocrinimmune (PNI) activity. The
 microarray is useful in diagnosing a condition associated with PNI

CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
 CC cancer and infection. The present sequence represents a
 CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
 CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
 CC SEQ ID NO 1829 are provided.

XX Sequence 1890 BP; 647 A; 377 C; 347 G; 519 T; 0 U; 0 Other;

Alignment Scores:

Score:	2,41e-303	Length:	1890
Percent Similarity:	3314.00	Matches:	626
Best Local Similarity:	99.5%	Conservative:	0
Query Match:	99.6%	Mismatches:	3
DB:	14	Indels:	0
		Gaps:	0

US-10-667-289-2 (1-629) X ADV43392 (1-1890)

QY 1 MetAen***ValThrIleGlnThrAenValIleAleuThrIleuPheSerTrp 20
 Db 1 ATGAATCAGGTCACTATTCATAGGAGATGCAATGATGCTTACATCTTCACTG 60
 QY 21 CysHisGlyGlyIleThraenIleAenCysSerGlyHisIleTrpValGlnProAleThr 40
 Db 61 TGTCAATGAGAAATTCAAATATTAATCTGCTGACCACTTGGATGAAACAGCCACA 120
 QY 41 IlePheIleMetGlyMetAenIleSerIleTyrCysGlnAleAleIleuAenCysGln 60
 Db 121 ATTTTAAGTGGATGATATCTCTATATATGCAAGACAGCAATTAAGACTCCAA 180
 QY 61 ProArgIleuHisPheTyrIleAenGlyIleuGlnArgPheGlnIleThraGlyIle 80
 Db 181 CCAAGAAACCTCATTTTATTAATAATGCAATCAAGAAAGATTTCAATTCACAAAGATT 240
 QY 81 AenIleThrThraIleArgLeuTrpTyrIleAenPheLeuGlnProHisIleSerMetTyr 100
 Db 241 AATTAACAAACAGCTGGCTTGGTATTAATCTTGGAAACCAATCTTATATGAC 300
 QY 101 CysThraIleGlnCysProIleHisPheGlnIleuThrLeuIleCysGlyIleAenPheSer 120
 Db 301 TGCATGCTGATGATGCTCCAAACATTTTCAAGAGACCTGATATGGAAGAAACATTTCT 360
 QY 121 SerGlyTyrProProAenPheIleProAenGlnValThrCysValIleTyrGlnIleSerGly 140
 Db 361 TCTGGATATCCGCAATATTTCTGATGAAGAAACCTGATGATATTAATATTCAGGC 420
 QY 141 AenMetThrCysThrThraPheAenIleHisPheLeuThrTyrIleAenPheTyrValIle 160
 Db 421 AACATGACTTGACCTCGAATGCTGGAAAGCTCACCTTACATAGACAAATATCGGTAT 480
 QY 161 HisValIleSerLeuGlnThrGlnIleuGlnIleuThrLeuThrSerSerTyrIleAen 180
 Db 481 CATGTGAAGATTTAGACAGAGAAAGAGCAACATATCTCACTCAAGCTATATTAAC 540
 QY 181 IleSerThraPheSerLeuGlnIleuGlyIleuTyrIleuValIleTrpValIleAenAen 200
 Db 541 ATCTCCACTGATTCATTAACAGGTGCAAGAGATCTTGTTGGTTCACAAACAGCAAC 600
 QY 201 AleuGlnMetGlnIleuSerIleuGlnIleuGlnIleHisLeuAenPheSerIleValIlePro 220
 Db 601 GCACTAGGATGAGAAAGTCAAAACATGCAATTCACCTGATATTAATGATATCT 660
 QY 221 SerAleAleValIleSerAenGlnIleuThrIleAenAleThraValProIleThraIle 240
 Db 661 TCTGAGCGGTATTTCCAGGCTGAGATTAATATGATGACAGTCCAAAGCAATATTT 720
 QY 241 TTTTPAeSerGlnThrThrIleGlnIleuValSerCysGlnMetArgTyrIleAenThr 260
 Db 721 TATTTGGATATGCAACAAATGAAAGGTTTCTCTGGAATGATGATGATGATGATGAT 780
 QY 261 ThraGlnThrThraAenValIleGlnIleuPheAenThraPheThrTyrValIleGlnIleuSer 280
 Db 781 ACAAACCAACTTGGATATTAAGATTTGAACCAATTTTACATATGCAACAGTCA 840

QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
 DB 841 GATTCTACTGAGCCAAACATTAGTACTGATTTCAAGTGAAGTCAAGAAACAGGC 900
 QY 301 LysArgTyrTrpGlnProTyrSerSerProPhePheHisLysThrProGluThrValPro 320
 DB 901 AAAAGGTACTGAGCCTTGAGTCTCACTGTTTTTCATTAACACCTGAAACAGTCCC 960
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
 DB 961 CAGGTACATCAAAAGCATTCACACATGACATGCAATTCGCGCTAACAGTTGCTTCC 1020
 QY 341 IleSerThrGlyHisIleuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
 DB 1021 ATCTCTACAGGGAACCTTACTTCTGACACAGAGAGACATTTGACTTTATTTGGAAATG 1080
 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
 DB 1081 ATCGCTTTGCTGTATGTTGTCATATCTTTCTTGATGGATATTACAGATCATTC 1140
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
 DB 1141 CGAACTGGGATTAAAGAGAGATCTTATGTTAATCAAAAGTGGCTTTATGAAGATATT 1200
 QY 401 ProAsnMetLysAsnSerAsnValValIleMetLeuGlnGluAsnSerGluLeuMetAsn 420
 DB 1201 CCTAATATGAAACACGCAATGTTGTGAATGCTACAGAAATAGTGAATCAATGAAT 1260
 QY 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440
 DB 1261 AATATTTCCAGTGAAGCGTCTTATATGTTGATCCCATGATTACAGAGATTAAGAATC 1320
 QY 441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
 DB 1321 TTCATCCAGAACACAGCCTACAGACTACAGAAAGAGATACAGACCCCTGAGACA 1380
 QY 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
 DB 1381 AGGACACACCGCAAACTCGCTATTCGACAAATACATGATGATATATCTCGATCTC 1440
 QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500
 DB 1441 AACACGTGGATATAACCCCAATTTTCAATTTCTGCTGAGGGAAGCCATCAGCAAT 1500
 QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
 DB 1501 AATATGAATTAATCTTCCTTAACACTTAACCAACAGTTGATTCCTTAAGACTCAGGAAT 1560
 QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
 DB 1561 AATCCCAAGGTTAAACAAAGCATCTTAATTTGCTTTTCTTTCAATGTGAATTCATCA 1620
 QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyLysSerSer 560
 DB 1621 AGCAACACATATTTCTTGAGAAATTAAGCCTCATATTAATCAAGAGAAATGCAATTCT 1680
 QY 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
 DB 1681 CTGACATCAAAACTCAGTAGAGAGAGAAACCAACATGCTTTTGGAAATGATTCAACC 1740
 QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
 DB 1741 AGTGAACATATTCAGAAACAGACCTGCTTCCTGATGAATTTGCTCTGTTGGGATC 1800
 QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
 DB 1801 GTGAATGAGAGTTGCGATCTATTAATCTTATTTTCCAAATAATTTTGGAAAGCCAC 1860
 QY 621 PheAsnArgIleSerLeuLeuGlyLys 629
 DB 1861 TTCAATGAGATTCACCTTGAAAG 1887

RESULT 5
 AAF87822
 ID AAF87822 standard; cDNA; 1910 BP.
 AC AAF87822;
 XX
 XX 11-JUL-2001 (first entry)
 DE Human haemopoietin receptor protein NR12.5 encoding cDNA SEQ ID NO:9.
 XX
 KW Human; haemopoietin receptor protein; NR12; immunosuppressive;
 KW antiallergic; haemopoietin factor; autoimmune disease; tissue rejection;
 KW metal allergy; pollen allergy; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1890
 FT /*tag= a
 FT /product= "NR12.5"
 FT /note= "haemopoietin receptor protein"
 XX
 PN MO200123556-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000MO-JP006654.
 XX
 PR 27-SEP-1999; 99JP-00273358.
 PR 03-AUG-2000; 2000JP-00240397.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PI Maeda M, Yaguchi N;
 XX
 DR WPI; 2001-266154/27.
 DR P-PDB; AAB74967.
 XX
 XX
 PT New hemopoietin receptor protein NR12 useful for screening for new
 PT binding factors for potential treatment of autoimmune disease, tissue
 PT rejection and allergies.
 XX
 PS Claim 1; Fig 13; 140pp; Japanese.
 XX
 CC The present sequence encodes a human haemopoietin receptor protein NR12
 CC designated NR12.5. NR12 has immunosuppressive and antiallergic
 CC activities. NR12 can be used for searching for haemopoietin factors with
 CC the potential for controlling autoimmune disease, tissue rejection and
 CC allergies against e.g. metals and pollen
 XX
 SQ Sequence 1910 BP; 654 A; 379 C; 352 G; 525 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,45e-303 Length: 1910
 Score: 3314.00 Matches: 626
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 3
 Query Match: 99.6% Indels: 0
 DB: 5 Gaps: 0
 US-10-667-289-2 (1-629) x AAF87822 (1-1910)
 QY 1 Metaasn***ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
 DB 1 ATGAATCAAGTCACTTTCATATGAGATGAGATAGCCCTTAACTACTCTTCACCTGG 60
 QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTyrValGluProAlaThr 40
 DB 61 TGTCAATGAGAGATTAACAATATTAATCTGCTGCGCAATCTGGGTAGAACCAACGACCA 120
 QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
 DB 121 ATTTTAAGATGGGTATGAATATCTTATATATGCAAGCAGCAATTAAGAATGCCAA 180

QY 61 ProArglyLeuHispheryTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
 Db 181 CCAAGGAACTTCATTTATATAAAATGCGATCAAGAAAGATTTCATATCAAGAGATT 240
 QY 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
 Db 241 AATTAACAACACACTCGCTTGGTATTAATAACTTCTCGAACACACTGCTTATGTAC 300
 QY 101 CysThrAlaGluCysProLysHisphGlnGluThrLeuIleCysGlyLysAspIleSer 120
 Db 301 TCGACTGCTAAAGTCCCAACATTTTCAAGAGACCTGATATGTGAAAGACATTTCT 360
 QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140
 Db 361 TCTGAAATATCCGCGAGATATTCCTGATGAAGTAACCTGTGCATTTATGAATTCAGCC 420
 QY 141 AsnMetThrCysThrTyrAsnAla***LysLeuThrTyrIleAspThrLysTyrValVal 160
 Db 421 AAGATGACTTGACCTGGAAATGCTGGAGAGCTCACCTACATAGCACAAATATCGTGTA 480
 QY 161 HisValLysSerLeuGluThrGluGluGluGlnGluThrLeuThrPheSerTyrIleAsn 180
 Db 481 CATGTGAAGCTTTAGAGACAGAAAGAGACACAGTATCTCACCTCAAGCTATATTAC 540
 QY 181 ILeSerThrAspSerLeuGlnGlyGlyLysLysTyrLeuValTyrValGlnAlaAlaAsn 200
 Db 541 ATCTCCACTATTCATTACAAAGGTGGCAAGAGATCTGTTGGGTCCAAAGCAGCAAC 600
 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLysLeuAspAlleValIlePro 220
 Db 601 GCACTAGGAGTGAAGAGTCAAAACCACTCAATTCACCTGGATGATATAGATGATCCT 660
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
 Db 661 TCTGAGCCCTCATTTCCAGGCTGAGACATTAATCTAAGTCCAGCCCAAGACCATATAT 720
 QY 241 TyrTyrAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
 Db 721 TATTTGGATAGTCAACACAAATTGAAGAGTTTCCGTGAATAGATCAAGGCTACA 780
 QY 261 ThrAsnGlnThrTyrAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
 Db 781 ACAAAACCAACTGGAATGTTAAAGATTGACCACTAATTTCATATGTGCAACAGTCA 840
 QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
 Db 841 GAAATCTACTTGAGCCAAACATTAAAGTACGTATTTCAAGTGAAGTCAAGAAACAGGC 900
 QY 301 LysArgTyrTyrGlnProTyrPheSerProPhePheHisLysThrProGluThrValPro 320
 Db 901 AAAAGGTACTGCGAGCCTTGSAGTCACTGTTTTTTCATATAAACCTGAAAACAGTTCCC 960
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTyrAsnSerGlyLeuThrValAlaSer 340
 Db 961 CAGGTCAATCAAAAGCATTCCAACATGACATGGAATTCGGGCTTAACAGTGTCTCC 1020
 QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyLysAspIleGlyLeuLeuGluMet 360
 Db 1021 ATCTCAACAGGCACTTACTCTTGACAAACAGAGACACATGTGACTTTATTTGGGAGATG 1080
 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
 Db 1081 ATGCTCTTCTGTTATGTGTGCTCAATCTTTCTTTGATGGGATATTAAACATCATTC 1140
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrLeuTyrGluAspIle 400
 Db 1141 CGAAGCTGGATTAAAGAGATCTTATGTATTAACAAAGGAGCTTTATGAAGATATT 1200
 QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420
 Db 1201 CCTAATATGAAAAACAGCAATGTTGTGAAAAATGCTACAGGAAAAATAGTGAATTAAT 1260

QY 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetCileThrGluIleLysGluIle 440
 Db 1261 AATTAATTCAGTGAAGAGGCTCATATGTTGATCCATGATTAACAAGATTAAGAAATC 1320
 QY 441 PheIleProGlnHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
 Db 1321 TTCTATCCAGAAACAAAGCCTACAGACTACAGAAAGAGATACAGAACCCCTGGAGACA 1380
 QY 461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
 Db 1381 AGAGACTACCCGGAAGAAACCTGCTATTCGACAAATACAGAGTTGATATATTCCTGATTC 1440
 QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLysSerAsn 500
 Db 1441 AACACTGGATATTAACCCCAATTTTCAAAATTTCTGCTGAGAGGAAAGCCATTCACATTAAT 1500
 QY 501 AsnAsnGluIleThrSerLeuThrLysProProValAspSerLeuAspSerGlyAsn 520
 Db 1501 AATTAATGAATTAATCTTCACTTAACACTTAACCAAGCTGATTCCTTAGCTCAGAAAT 1560
 QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
 Db 1561 AATCCAGGTACAAAGACATCCTATTTTGTCTTTCTGTTCAAGTGTGAATTCACAT 1620
 QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyGlyCysSerSer 560
 Db 1621 AGCAACACAAATATTTCTTGAGATTAAGCTTCATATTAATCAAGAGAAATGCAATCTCT 1680
 QY 561 ProAspIleGluAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
 Db 1681 CCTGACATCAAAACCTCAGTAGAGAGAGAAACCAACATGTTTGGAAATGATCAACC 1740
 QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
 Db 1741 AGTGAACATATTCACAAACAGACCTCCTTCGATGAATTTGTCTCCGTTGGGAGATC 1800
 QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
 Db 1801 GTGATGAGAGAGTGCATCTATTAATTAATTTTCCAAAAATATTTTGGAAAGCCAC 1860
 QY 621 PheAsnArgIleSerLeuLeuGluLys 629
 Db 1861 TTCAATGAGATTCACCTTGGAAAAAG 1887
 DE RESULT 6
 ID AAD38773 standard; cDNA; 2830 BP.
 AC AAD38773;
 XX 23-SEP-2002 (first entry)
 DE Human haematopoietin receptor 2 (HPR2) cDNA.
 XX Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;
 XX pancytopenia; leukopenia; anemia; thrombocytopenia; osteoporosis;
 XX neurodegenerative disorder; leukemia; carcinoma; haematologic disorder;
 XX cancer; myeloid/plastic syndrome; idiopathic thrombocytopenic purpura;
 XX ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 XX osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
 XX anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 XX demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 XX vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 XX stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 XX lechaemic disease; gene; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 107..1996
 FT /tag= a
 FT /product= "Human HPR2 protein"
 FT /note= "this region is specifically claimed as SEQ ID NO:

FT sig_peptide 20 in claim 9 of the specification"
 FT 137. .175
 FT /*tag= b
 FT mat_peptide 176. .1993
 FT /*tag= c
 FT variation /product= "Human mature HPR2 protein"
 FT replace(1035, C)
 FT /*tag= d
 FT variation replace(2172, G)
 FT /*tag= e
 PN WO200229060-A2.
 PD 11-APR-2002.
 PF 05-OCT-2001; 2001MO-US031634.
 PR 06-OCT-2000; 2000US-0238706P.
 PR 13-OCT-2000; 2000US-0240476P.
 PR 20-FEB-2001; 2001US-0270282P.
 XX (IMM) IMMUNEX CORP.
 PA Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 PI P-PSDB; AAE24033.
 DR WPI; 2002-330172/36.
 XX P-PSDB; AAE24033.
 PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions.
 PS Claim 9; Page 117-119; 136pp; English.
 XX The present invention relates to human and murine hematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukemia and tumor
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various hematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), hematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as
 CC osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence is
 CC human HPR1 cDNA
 SO Sequence 2830 BP; 922 A; 574 C; 551 G; 783 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.27e-303 Length: 2830
 Score: 3314.00 Matches: 626
 Percent Similarity: 99.5% Conservative: 0

Best Local Similarity: 99.5% Mismatches: 3
 Query Match: 99.6% Indels: 0
 DB: 6 Gaps: 0
 US-10-667-289-2 (1-629) x AAD38773 (1-2830)
 QY 1 MetAsn***ValThrIleGlnTPAaPAlaValIleAlaLeuTyrIleLeuPheSerTyr 20
 Db 107 ATGAATCAGGCTCACTATTCATTCAGATGAGATGACGATATGACCTTTACATCACTTCAGCTGG 166
 QY 21 CysHisGlyGlyIleThrAsnIleAsnGlySerGlyHisIleTyrValGluProAlaThr 40
 Db 167 TGTCAATGAGGAAATTCATAATATAAATGCTGTGGCCACATCGGGTAGAACAGCCACA 226
 QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaIleLysAsnGlyGln 60
 Db 227 ATTTTAAAGTGGATGATATCTTATTTATTTATTTGCGAACGACCAATTAAAGACTGCCAA 286
 QY 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
 Db 287 CCAAGGAACCTTCATTTTATATAAATGGCATCAAGAAAGATTTCATCAACAGAGATT 346
 QY 81 AsnLysThrThrAlaArgLeuTyrLysAsnPheLysGluProHisAlaSerMetTyr 100
 Db 347 AATTAACAAACAGCTGGCTTTGTATATAAACTTTCTGGAACACATGCTTATGTATAC 406
 QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
 Db 407 TGCACCTGTAATGCTCCAAACATTTTCAGAACACCTGATATGTAAGAAACATTTCT 466
 QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140
 Db 467 TCTGATATCCGCAATATTCCTGATGAAGTACCTGTCTATATGATATTTCAAGGC 526
 QY 141 AsnMetThrCysThrTyrAsnAla***LysLeuThrTyrIleAspThrLysTyrValVal 160
 Db 527 AACATACCTTGACCTCGAATGCTGGAAAGCTCACCTACATACCAAAATACGTGGTA 586
 QY 161 HisValLysSerLeuGluThrGluGluGluGlnGluThrLeuThrSerSerTyrIleAsn 180
 Db 587 CATGTAAAGATTTAAGACAGAAAGAGCAACAGATCTCACTCACTCACTCACTCACTCACT 646
 QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGlnAlaAsn 200
 Db 647 ATTCATCACTGATTCATTCACAGTGCACAGTACATCTGTTGGGTCCAGACAGCAAC 706
 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
 Db 707 GCACTAGGATGGAGAGTCAAAACATGCAAAATTCACCTGGATGATATAGATACCT 766
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
 Db 767 TCTGCAAGCCGTATTTCCAGGGCTGAGCTATTAAGCTACAGTGCACCAAGCAATTAAT 826
 QY 241 TyrTyrAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
 Db 827 TATTGGATATGTCACCAACCAATTTAAAGTTTCTGTGAATGATACAGGCTACA 886
 QY 261 ThrAsnGlnThrTyrAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
 Db 887 ACAACCAAACTTGAAATGTAAAGATTTGACCAATTTTCATATATGCAACAGTCA 946
 QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
 Db 947 GAATTTACTTGGAGCAAAACATTAAGTACGATTTCAAGTGAAGTCAAGAAACAGGC 1006
 QY 301 LysArgTyrTyrGlnProTyrPheSerPhePheHisLysThrProGluThrValPro 320
 Db 1007 AAAAGTACTGCAAGCTTGAGCTTCACTGTTTTCATTAACACATCAAGTATCC 1066
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTyrAsnSerGlyLeuThrValAlaSer 340
 Db 1067 CAGGTCAATCAAAACATTCACATGACATGAGATTTCTGGGCTAACAGTTCCTCC 1126

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QY 341 ILeSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
DB 1127 ATCTTACAGAGGACCTTACTTTCGACACAGAGGACATTTGGACTTTATTTGGGAATG 1186
QY 361 ILeValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
DB 1187 ATGCTCTTCTGTTATGATGTTGCAATCTTCTTGTGATTTGGAATATTTAAACAGATCAATTC 1246
QY 381 ArgThrGlyIleIleValArgArgIleLeuLeuLeuIleProIleThrLeuIleArgIle 400
DB 1247 CGAACTGGGATTTAAAGAGAGATCTTATGTTAAATACCAAGTGGCTTTATGAAAGATAT 1306
QY 401 ProAsnMetIleValAsnSerAsnValValIleMetLeuGlnIleAsnSerGlyLeuMetAsn 420
DB 1307 CTTATATGAAAAACAGCAATGTTGTGAAAATGTCACAGAAAATGTCAGAACTTATGAAAT 1366
QY 421 AsnAsnSerSerGlnIleValIleValIleAspProMetIleThrGlyIleIleGlyIle 440
DB 1367 AATTAATTCAGTGAAGAGTCTCTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1426
QY 441 PheIleProGlnIleIleValSerProThrAspTyrIleValGlyLeuSerThrGlyProLeuGluThr 460
DB 1427 TTCATCCCAAGACAAAGCCTTACAGACTACAGAGAGAGATACAGAGACCCCTGGAGACA 1486
QY 461 ArgAspTyrProGlnAsnSerIlePheAspAsnThrThrValValIleIleProAspLeu 480
DB 1487 AGGAGTACCCCGGAAAATCTGCTATTCGACATATCTACATGATATATCTCTGATCTC 1546
QY 481 AsnThrGlyTyrIleProGlnIleSerAsnPheLeuProGlnIleSerHisLeuSerAsn 500
DB 1547 AACACTGATATATAACCCCAATTTCTCAATTTCTGCTGAGGAGAACCTTCACGCAAT 1606
QY 501 AsnAsnGlnIleThrSerLeuThrIleValProValAspSerLeuAspSerGlyAsn 520
DB 1607 AATTAATGAAATTAATCTTCTTAACACTTAACACACCACTTAATCTTGACTCAGGAAT 1666
QY 521 AsnProArgLeuGlnIleValIleProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
DB 1667 AATCCCAAGTTACAAAGCATCTCAATTTGCTTTTCTGTTCAATGTAATTCATCTA 1726
QY 541 SerAsnThrIlePheLeuGlyIleLeuSerLeuIleLeuAsnGlnIleGlyCysSerSer 560
DB 1727 AGCAACACATATATTTCTTGAGAAATTAAGCTCATATTAATCAAGAGAAATCAGATCTT 1786
QY 561 ProAspIleGlnAsnSerValGlnGlnIleThrThrMetLeuGlnIleAsnAspSerPro 580
DB 1787 CTTGACTACAAACCTCAGTGAAGAGAGAAACCAACATGCTTTGAAAAATGATTCACC 1846
QY 581 SerGluThrIleProGlnIleThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
DB 1847 AGTGAACATTTCTCAAGAACAGACCCCTGCTCTGATGAATTTGCTCTCTTTGGGATC 1906
QY 601 ValAsnGlnIleLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnSerHis 620
DB 1907 GTGAATGAGAGATGCGCATATTAATCTTATTTCCACAAATATTTGAAAGCCAC 1966
QY 621 PheAsnArgIleSerLeuLeuGlyIle 629
DB 1967 TTCAATAGGATTTCACTTGAAGAAAG 1993

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KM metal allergy; pollen allergy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 98..1987
FT /tag= a
FT /product= "NR12.3"
FT /note= "haemopoietin receptor protein"
XX
PN M0200123556-A1.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000MO-JP006654.
XX
PR 27-SEP-1999; 99UP-00273358.
PR 03-AUG-2000; 2000UP-00240397.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Yaguchi N;
XX
DR WPI; 2001-266154/27.
DR P-PSDB; AAB74965.
XX
XX
PT New hemopoietin receptor protein NR12 useful for screening for new
PT binding factors for potential treatment of autoimmune disease, tissue
PT rejection and allergies.
XX
PS Claim 1; Fig 6; 140pp; Japanese.
XX
CC The present sequence encodes a human haemopoietin receptor protein NR12
CC designated NR12.3. NR12 has immunosuppressive and anti-allergic
CC activities. NR12 can be used for searching for haemopoietin factors with
CC the potential for controlling autoimmune disease, tissue rejection and
CC allergies against e.g. metals and pollen
XX
SQ Sequence 2123 BP; 731 A; 419 C; 395 G; 578 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No. 3.44e-301 Length: 2123
Score: 3292.00 Matches: 622
Percent Similarity: 99.2% Conservative: 2
Best Local Similarity: 98.9% Mismatches: 5
Query Match: 99.0% Indels: 0
DB: Gaps: 0

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US-10-667-289-2 (1-629) x AAF87820 (1-2123)

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QY 1 MetAsn***ValThrIleGlnIleThrPheAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
DB 98 ATGATCAAGTCACTTCTTAATGGAATGCAAGTAAATGACCTTTACATCTTCACTG 157
QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleIleTrpValGlnProIleThr 40
DB 158 TGTCAATGAGAAATTAACAATATTAATCTGCTGCGCACATCTGGGTAAGAACAGCACA 217
QY 41 ILePheIleMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleIleValAsnCysGln 60
DB 218 ATTTTAAGATGGGTGGAATATCTATATATTTGCAAGCACAAATTAAGAACTGCCAA 277
QY 61 ProArgIleLeuHisPheTyrIleValAsnGlyIleIleValGlnIleThrPheGlnIleThrArgIle 80
DB 278 CCAAGAACTTCATTTTATTAATAATGGCATCAAGAAAGATTTCAATCAAGGATT 337
QY 81 AsnIleThrThrAlaArgLeuTyrTyrIleAsnPheLeuGluProHisAlaSerMetTyr 100
DB 338 AATTAACAAACAGCTGCGCTTGGTATTAATAAATCTTCTGGAACACATGCTTCTATGTAC 397
QY 101 CysThrAlaGlnCysProIleHisPheGlnIleThrLeuIleCysGlyIleValAspIleSer 120
DB 398 TGCACGTGGAATGTCCAAACATTTTCAAGAGACCTGATATGTGAAAAAGCATTTCT 457

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QY 121 SerGIYrProProaspIleProaspGluValThrCysValIleIleYrGIuYrSerGIY 140
 DB 458 TCGGATATCCGCGACAGATATTCCTGATGAAAGTAACCTGTCTATTATGATATTCAGGC 517
 QY 141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTYrIleAspThrIleYrValVal 160
 DB 518 AATCATGACCTGCACCTGGAAATGCTGGAGAGCTCACCTACATAGACAAATAATAGTGTGA 577
 QY 161 HisValLysSerLeuGIuThrGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 180
 DB 578 CAGTGAAGAGTTAGAGACAGAAAGAACCAAGATCTCACTCAACCTATATTAAAC 637
 QY 181 IleSerThrAspSerLeuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 200
 DB 638 ATCTCCACGATTCATTACAGAGTGGCAAGAGTACTGGTTGGGTCCAGACAGCAAAC 697
 QY 201 AlaLeuGIuMetGIuGIuSerIleGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 220
 DB 698 GCACAGGAGCATGAGAGAGTCAAAACCACTGCAATTCACCTGGATGATATAGATGACTT 757
 QY 221 SerIleAlaValIleSerArgIleGIuThrIleAsnAlaThrValProIleThrIleIle 240
 DB 758 TCTGACGCCGTCATTCAGGGCTGAGACATTAATGCTACAGTGCACCAAGACCATATT 817
 QY 241 TYrTrpAspSerGIuThrTrIleGIuLysValSerCysGIuMetArgTYrLysAlaThr 260
 DB 818 TATTGGATATGTCAACACAAATTGAAAGAGTTTCTGTAAATGAGATTCAGAGCTACA 877
 QY 261 ThrAsnGIuThrTrpAsnValLysGIuPheAspThrAsnPheThrTYrValGIuGIuGIu 280
 DB 878 ACAACCAAACTTGAAATGTTAAAGATTTGACACCAATTTTACATATGTCAGCAACGTCA 937
 QY 281 GluPheTYrLeuGIuProAsnIleIleTYrValPheGIuValArgCysGIuGIuGIuGIu 300
 DB 938 GAATTCATCTTGAGGCCAAACATTAAGTACGTATTTCAAGTGAAGTCAAGAAACAGGC 997
 QY 301 LysArgTYrTrpGIuProTrpSerSerProPhePheIleIleThrProGIuThrValPro 320
 DB 998 AAAAGGTACTGGAGCCCTTGAAGTTCCTGTTTTCATTAACCACTGAAACAGTTCCC 1057
 QY 321 GluValThrSerLysAlaPheGIuIleAspThrTrpAsnSerGIuLeuThrValAlaSer 340
 DB 1058 CAGTCACATCAAAAGATTCACAAATGACACATGGAATTCGGGGCTTAACAGTTGCTTC 1117
 QY 341 IleSerThrGIuIleIleuThrSerAspAsnArgIleAspIleGIuLeuLeuGIuMet 360
 DB 1118 ATCTCAACAGGGCACCTTACTCTGACMACAGAGGAGACATTTGACTTTATTTGGGATG 1177
 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGIuIlePheAsnArgSerPhe 380
 DB 1178 ATGCTCTTGTCTGTATGTGTGATCTTCTTTGATGTGGACATTTTACAGATCATTTTC 1237
 QY 381 ArgThrGIuIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTYrGIuAspIle 400
 DB 1238 CGAAGCTGGGATTTAAAGAGATCTTATGTTATACCAAGTGGCTTATAGAGATATT 1297
 QY 401 ProAsnMetLysAsnSerAsnValLysMetLeuGIuLysAsnSerGIuLeuMetAsn 420
 DB 1298 CCTTAATATGAAAAACAGCATGTGTGTAATATCTACAGGAAATAGTGAATTAAGAAAT 1357
 QY 421 AsnAsnSerSerGIuGIuValLeuTYrValAspProMetIleThrGIuIleLysGIuIle 440
 DB 1358 AATTAATTTCCAGTAGAGGCTCTATATGTATGATCCCATGATACAGAGATTAAGAAATC 1417
 QY 441 PheIleProGIuIleIleLysProThrAspTYrLysLysGIuAsnThrGIuProLeuGIuThr 460
 DB 1418 TTGATCCGAGAACACAAAGCTTACAGACTACAAAGAGAGAAATACAGGACCCCTGGAGACA 1477
 QY 461 ArgAspTYrProGIuAsnSerLeuPheAspAsnThrThrValValTYrIleProAspLeu 480
 DB 1478 AGAGACTACCCGCAAACTGCTATTCGACAAATACACAGTGTATATATATCTGATCTC 1537

QY 481 AsnThrGIuTYrLysProGIuIleSerAsnPheLeuProGIuIleSerHisLeuSerAsn 500
 DB 1538 AACACGGATATATACCCCAATTTCTGCTGAGGGAGACATTCAGTAT 1597
 QY 501 AsnAsnGIuIleThrSerLeuThrLysProProValAspSerLeuAspSerGIuAsn 520
 DB 1598 AATTAATGAATATCTTCCCTTAACACTTAAACACAGTGTATCTTAGACTCAGGAAAT 1657
 QY 521 AsnProArgLeuGIuIleHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
 DB 1658 AATCCAGGTTACAAAGACATCTTAATTTGCTTTTCTGTTCAGAGTGAATTCACCTA 1717
 QY 541 SerAsnThrIlePheLeuGIuLysLeuSerLeuIleLysAsnGIuGIuGIuGIuGIuGIu 560
 DB 1718 AGCAACACAAATTTCTTGAGAAATTAAGCTCATATTAAATCAGAGAGATCAGATTCT 1777
 QY 561 ProAspIleGIuAsnSerValGIuGIuGIuThrThrMetLeuGIuLysAsnAspSerPro 580
 DB 1778 CCTGACATACAAACCTCAGTAGAGAGAAACACACATGCTTTTGGAAATGATTCACCC 1837
 QY 581 SerGIuThrIleProGIuGIuThrLeuLeuProAspGIuPheValSerCysLeuGIuIle 600
 DB 1838 AGTGAACATATTCACAGAACAGACCTGCTTCGTATGAATTTGCTCTGTTGGGATC 1897
 QY 601 ValAsnGIuGIuLeuProSerIleAsnThrTYrPheProGIuAsnIleLeuGIuSerHis 620
 DB 1898 GTGAATGAGAGTGGCATCTATTAATCTTATTTCCACAAATATTTTGGAAAGCCAC 1957
 QY 621 PheAsnArgIleSerLeuLeuGIuLys 629
 DB 1958 TTCAATAGCATTTCACTCTTGAAAG 1984
 DB 23-SEP-2002 (first entry)
 DE Human haematopoietin receptor 2 (HPR2) ex8-ex9 DNA.
 XX
 XX AAD38774;
 AC AAD38774 standard; DNA; 1698 BP.
 ID AAD38774
 DT 23-SEP-2002 (first entry)
 XX
 XX Human haematopoietin receptor 2 (HPR2) ex8-ex9 DNA.
 DE
 XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
 KW pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;
 KW neurodegenerative disorder; leukaemia; carcinomas; haematologic disorder;
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KW osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KW ischaemic disease; gene; ds.
 KW
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT 1..1698
 FT CDS /tag= a
 FT /product= "Human HPR2 ex8-ex9 protein"
 PN MO200229060-A2.
 PD 11-APR-2002.
 XX
 XX 05-OCT-2001; 2001WO-US031634.
 PF 06-OCT-2000; 2000US-0238706P.
 PR 13-OCT-2000; 2000US-0240476P.
 PR 20-FEB-2001; 2001US-0270282P.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA XX

PI Cosman DJ, Moseley BA, Bird TA, Dubose RF, Wiley SR;
 XX WPI; 2002-330172/36.
 DR P-PSDB; AAE24034.
 XX
 PT Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions.
 XX
 PS Claim 9; Page 123-124; 136pp; English.
 XX
 CC The present invention relates to human and murine hematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukemia and tumor
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various hematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasoocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as
 CC osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence is
 CC human HPR2 ex8-ex9 DNA
 XX
 SQ Sequence 1698 BP; 597 A; 335 C; 310 G; 456 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,89e-269 Length: 1698
 Score: 2952.00 Matches: 562
 Percent Similarity: 89.3% Conservative: 0
 Best Local Similarity: 89.3% Mismatches: 3
 Query Match: 88.8% Indels: 64
 Gaps: 1
 US-10-667-289-2 (1-629) x AAD36774 (1-1698)
 QY 1 MetAsn**ValThrIleGlnTPAspAlaValIleAlaLeuTYrIleLeuPheSerTyr 20
 Db 1 ATGATCAGGTCACTATTCATATGAGATGAGATATATACCCCTTATCATATCTTCAGCTGG 60
 QY 21 CyeHisGlyGlyIleThrAsnIleAsnCySerGlyHisIleTyrValGluProAlaThr 40
 Db 61 TGCATCGAGGAATTACAAATATATTAATGCTCTGGCCACATCTGGGTGAACAACGACCA 120
 QY 41 IlePheIleMetGlyMetAsnIleSerIleTyrCysGlnAlaIleIleLeuAsnCyGln 60
 Db 121 ATTTTAAAGATGGATGAATATCTCTATATATTCAGACAGCAATTAAGAACTGCAA 180
 QY 61 ProArgIleLeuHisPheTYrIleAsnGlyIleIleGlyIleArgPheGlnIleThrArgIle 80
 Db 181 CCAAGGAATCTTCACTTTTATTAATAAATGCGATCAAAAGAAATTTCAAAATCAAGATTT 240
 QY 81 AsnIleThrThrAlaArgLeuTyrTYrIleAsnPheLeuGluProHisAlaSerMetTyr 100

Db 241 AATTAACCAACACAGCTGGCTTGGTATTAACAACTTCTGGAAACCAATGCTTATGTAC 300
 QY 101 CyeThrAlaGluCyProIleHisPheGlnGluThrLeuIleCysGlyIleAspIleSer 120
 Db 301 TGCATCGCTGAATATGTCACAAACATTTTCAAGAGACACTGATATGTGAAAAGCATTTCT 360
 QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
 Db 361 TCTGATATCCCGCAGATATTCCTGATGAAGTAACCTGTGTCTATTAATGATATTCAGGC 420
 QY 141 AsnMetThrCysThrThrPheAsnAla***IleLeuThrTyrIleAspHisTyrValIle 160
 Db 421 AACATACCTTGACCTCGGAATGTGGGAAGCTCACCATCAATACACAAATACGTGGTA 480
 QY 161 HisValIleSerLeuGluThrGluGluGluGlnGlnIleTyrLeuThrSerSerTyrIleAsn 180
 Db 481 CATGTGAAGAGTTTAAAGACAGAAAGAGCAACATATCTCCCTCAAGCTATATTAAAC 540
 QY 181 IleSerThrAspSerLeuGlnGlyIleIleIleValIleTyrValGluAlaAlaAsn 200
 Db 541 ATCTCCACGATTCATTACAGAGGTGGCAAGATCTGTGGTCCCAAGCAAGCAAAAC 600
 QY 201 AlaLeuGlyMetGluGluSerIleGluGlnIleHisLeuAspAspIleValIlePro 220
 Db 601 GCACTAGGCAATGGAAGATCAAAACATGCAAAATTCACCTGATATATATGATACCT 660
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProIleThrIleIle 240
 Db 661 TCTGCAAGCGTCACTTTCCAGGCGTGAAGCATTAATAGCTACAGTCCCAAGCATTAAT 720
 QY 241 TyrTyrAspSerGlnThrIleGlyIleValIleSerCysGluMetArgTyrValAlaThr 260
 Db 721 TATTTGGATATGTAAACCAATTTGAAAAGTTCTCTGGAAATVAGATACCAAGCTTACA 780
 QY 261 ThrAsnGlnThrThrAsnValIleGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
 Db 781 ACAAAACCAACCTTGAATGTAAAGATTTGACCAATTTTACATATGTGCAACAGTCA 840
 QY 281 GluPheTyrLeuGluProAsnIleIleIleTyrValIlePheGlnValArgCysGlnGluThrGly 300
 Db 841 GAATTTCACTTGAAGCCAAACATTAAGTACGATTTTCAAGTGAAGTCAAGAAACAGCG 960
 QY 301 IysArgTyrTyrGlnProTyrSerSerProPhePheHisIleTyrProGluThrValPro 320
 Db 901 AAAAGTACTGCGACGCTTGAAGTTCACTGTTTTTTCATTAACACACTGAA----- 951
 QY 321 GlnValThrSerIleAlaPheGlnHisAspThrTyrAsnSerGlyLeuThrValAlaSer 340
 QY 951 ----- 951
 QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
 Db 951 ----- 951
 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
 Db 951 ----- 951
 QY 381 ArgThrGlyIleIleYsArgArgIleLeuLeuLeuIleProIleTyrPheLeuTyrGluAspIle 400
 Db 952 ---ACAGGATTAAGAAAGAGATCTTATGTTATATCAAAAGTGGCTTTATGAAAGATTT 1008
 QY 401 ProAsnMetCysAsnSerAsnValIleIleMetLeuGlnIleAsnSerGluLeuMetAsn 420
 Db 1009 CTTAATATGAAAACACGCAATGTTGTGAAAATCTCAAGAAAATAGTGAACCTTAATGAAT 1068
 QY 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleIleGlyIle 440
 Db 1069 AATTAATTCAGTGAAGAGGCTTATATGTGAATCCCATGATTCACAGATTAAGAAATTC 1128
 QY 441 PheIleProGluHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1188

[illegible]

PT	receptor complex for p40/IL-830, useful for treating conditions
PT	associated with abnormal expression or triggering of response to p40/IL-
PT	B30 ligand.
XX	
XX	
PS	Disclosure; Page 13; 74pp; English.
CC	
CC	The present DNA sequence represents a reverse translation of the human
CC	DNM cytokine receptor subunit 5 (defined as DCR55 or IL30 receptor) of
CC	the invention. DCR55 is a member of the class I branch of the cytokine
CC	receptor superfamily and is closely related to the IL-6 receptor subunit
CC	gp130 and the IL-12 β -Beta-2 subunit. Cytokines are soluble molecules
CC	which play a critical role in controlling the complex cellular
CC	interactions of the immune response. The invention comprises novel
CC	receptors related to cytokine receptors designated DNM cytokine receptor
CC	subunits (DCRS). Specifically the invention comprises a subunit (DCRS5)
CC	for a receptor complex for the p40/IL-B30 ligand. The DCR5 proteins of
CC	the invention are useful for treating diseases or disorders associated
CC	with abnormal expression or abnormal triggering of response to the p40/IL-
CC	B30 ligand. The proteins of the invention can be used to modulate the
CC	physiology or development of a cell from a host which exhibits Th1-
CC	mediated disease; multiple sclerosis; rheumatoid arthritis;
CC	osteoarthritis; inflammatory bowel disease; diabetes; psoriasis; sepsis;
CC	an allogeneic transplant recipient; chronic Th2 response; tumour; viral or
CC	fungal growth; vaccine recipient; or an allergic response
XX	
RSQ	Sequence 1807 BP; 421 A; 103 C; 245 G; 257 T; 0 U; 781 Other;
Alignment Scores:	
Pred. No.:	1,166-249
Score:	2747.00
Percent Similarity:	80.3%
Best Local Similarity:	80.3%
Query Match:	82.6%
DB:	6
	Gaps: 0
	Length: 1887
	Matches: 505
	Conservative: 0
	Mismatches: 124
	Indels: 0
	Gaps: 0

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Oy      1 MecAen***ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
Db      1  ATGAAGACAGTGNACNATCATGACGAGCGCGTGNATATGTCNVTATATATTTTNTTNTG 60
Oy      21  CySHASGIYGIYIleThrAsnIleAsnCySerSerGIYHISleTrpValGluProAlaThr 40
Db      61  TGYCAGGAGGAGATACNAAATATHAATYGYWSNGGNCATATHTGGGTGNARCCNGCNACN 120
Oy      41  IlePheYSMeGIYMeCAsnIleSerIleTyrCYSGInAlaAlaIleYsaenCYGIn 60
Db      121  ATHTTAAATATGGGATGAAATATHSMNATHTAYTGYCARGCGCGCNTTAAARAATGYCAR 180
Oy      61  ProAGlySleuHISpHeTyrIlyAsnGlyIleYsGIuAaRGheGlnIleTrpAaGIIe 80
Db      181  CCNMGNARATYTCATTTTAAARAAYGGNATHAARGAMGNITTYCARATHACNMGNAH 240
Oy      81  AsnYSerThrThrAlaArgLeuTrpTyrIlySaenPheLeuGluProHISaIaSerMeTyr 100
Db      241  AAYARACNACNCGMAGNVTNTGTATARAARAATYTTNTGARCCNCAAYCGMSENAITGTA 300
Oy      101  CySThrAlaGluCySProlYSHISpHeGInGluThrLeuIleCySGIlyYSaPIIeSer 120
Db      301  TGYACNCGNGARTGYCCNAAARCAATYTYCARGARACNATATGTGCGNARAGYATHTMSN 360
Oy      121  SerGIYTrpProPAsPIleProAspGluValThrCyValIleTyrGIuTyrSerGIY 140
Db      361  WSNGTATYCCNCGNAGATHTCCNAGYARGRGINACTGTGTATHTATYAGARTWWSNGN 420
Oy      141  AsnMeTyrCySThrTrpSnaIa**LYSLeuThrTyrIleAspThrIlySTyrValVal 160
Db      421  AAYATGACNCTGTACNTGGAAYCGMGNARATYTNACTATATATGAYACNAAARTAYGNGTN 480
Oy      161  HISValIySerLeuGluThrGIuGluGluGInGlnTyrLeuThrSeSerTyrIleAsn 180
Db      481  CAYGTNAARMSYNTMGARACNARGARARCARCAARTATYTNACMNSMNSNTATATHAAY 540

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QY 281 GluPheTyrLeuGluProAsnIleValPheGlnValArgCysGlnIuThrGly 300
 Db 938 GAATTTACTGAGCCAAACATTAAGTATTTCAAGTAGATGTCAAGAAACAGGC 997
 QY 301 LysArgTyrTrpGlnProTyrPheSerProPheMetIleYerThrProGlnIuThrValPro 320
 Db 998 AAAAGGTACCTGGCCCTTGGAGTTCAGTCTGTTTTCATAAACACCTGAACAGTTC 1057
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
 Db 1058 CAGGTCACTCAAAAGCATTCACACATGACATGAGATTCCTGGCTTACAGTTCCTCC 1117
 QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
 Db 1118 ATCTCTACAGGCGACCTTACTTCTGACACAGAGACATTTGACTTTATTGGGATG 1177
 QY 361 IleValIleAlaValMetLeuSerIleLeuSerIleGlyIlePheAsnArgSerPhe 380
 Db 1178 ATCTCTTGTCTGTATGTTGTCAATCTTCTTGTGATGGATATTAAACAGATCATTC 1237
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGlyAspIle 400
 Db 1238 CGAAGCTGAGATTAAAGAGAGATCTTATTTATACCAAGTGGCTTTATGAAGATATT 1297
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 RESULT 13
 AAC88149
 ID AAC88149 standard; cDNA; 1155 BP.
 AC AAC88149;
 XX 13-MAR-2001 (first entry)
 DT
 XX
 DE Human DNAX cytokine receptor subunit-2 encoding cDNA SEQ ID NO:1.
 XX
 KW Human; DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WC0200073451-A1.
 PD 07-DEC-2000.
 XX
 PF 30-MAY-2000; 2000MO-US014867.
 XX
 PR 01-JUN-1999; 99US-00322913.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
 XX WPI; 2001-061536/07.
 DR P-PSDB; AAB36646.
 PT Novel composition comprising DNAX cytokine receptor subunit polypeptide
 XX immunological disorders.
 XX
 PS Claim 16; Page 10-11; 93pp; English.
 XX
 CC The present invention describes a composition (I) comprising a
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The
 CC DCRS2 polypeptide is useful for binding ligands and for preparing
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for detecting
 CC presence of their ligands and in drug screening assays. It is also useful
 CC for treating conditions such as immunological disorders. The present

CC sequence encodes the human DCRS2 protein
 SQ Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 6,19e-183 Length: 1155
 Score: 2039.00 Matches: 382
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 QY 181 IleSerThrAspSerLeuGlnIuGlyLysTyrLeuValTrpValGlnAlaAsn 200
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 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
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 Db 781 ACAACCAAACTGGAGATGTTAAAGAAATTTGACACCAATTTTCAATATGCAACAGTCA 840
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Db      721  TATTGGATGTGTAACAACATTAAGGATTCCTGTGAATGAGATTCACAGGCTTACA
Qy      261  ThrAsnGlnThrTrpAsnValIleGlnPheAspThrAsnPheThrTyrValIleGlnIleSer
Db      781  ACAACCAACTGGATGTTAAAGATTTGACCCCAATTTTACATATGTCACCAAGCTCA
Qy      281  GluPheTyrIleGlnIleProAsnIleValTyrValIlePheGlnValIleArgCysGlnIleThrGly
Db      841  GAATTCCTAATGAGCCAAACATTAAGTACGTAATTCAGTGAATGATGTCAGAAACAGGC
Qy      301  LysArgTyrTrpGlnProTyrSerSerProPhePheHisIleValThrProGlnThrValPro
Db      901  AAAAGGACTGGACGCTTGAGTTCCAGTTCCCGTTTTCATTAACACCTGAAACAGTTCCC
Qy      321  GlnValIleSerIleValIlePheGlnIleAspThrTrpAsnSerGlyLeuThrValIleSer
Db      961  CAGGTCAATCAAAAGCATTCACATGACATGACATGGAATTCGGGCTTAACAGTTGCTTCC
Qy      341  IleSerThrGlyIleIleLeuThrSerAspAsnArgGlyValIleGlyLeuLeuLeuGlyMet
Db      1021 ATCTCTACAGGCGCACTTACTTCTGACACAGAGACATGGAATTCGACTTTAATGGGATG
Qy      361  IleValPheIleValIleMetLeuSerIleLeuSerIleIleGlyIlePheAsnArgSerPhe
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RESULT 15

AD265011 ID AD265011 standard; DNA; 1155 BP.

AD265011;

28-JUL-2005 (first entry)

DNAX cytokine receptor subunit 2 (DCRS2) DNA, seq id 1.

Immunomodulator; cell growth; DNAX cytokine receptor subunits 2; DCRS2;

immune disorder; gene; ds.

Primates.

Location/Qualifiers

1. 1155

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1. 69

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70. 1152

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US2005106673-A1.

19-MAY-2005.

17-DEC-2004; 2004US-00016106.

01-JUN-1999; 99US-0137159P.

31-MAY-2000; 2000US-00588113.

18-SEP-2002; 2002US-00247463.

(SCHE) SCHERING CORP.

Dowling LM, Timane JC, Gorman DM, Kastelein RA, Bazan JF;

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XX      WPI; 2005-365817/37.
DR      P-PSDB; AD265012.
XX      Composition useful for diagnosing or creating immunological disorders,
PT      comprising pure or recombinant DNAX cytokine receptor subunits 2 (DCRS2)
PT      polypeptide or its fusion polypeptide.
XX      Disclosure; SEQ ID NO 1; 42pp; English.
XX      The invention relates to a composition (I) of matter chosen from a
CC      substantially pure or recombinant DNAX cytokine receptor subunit 2
CC      (DCRS2) polypeptide. Further disclosed is a substantially pure or
CC      isolated antigenic DCRS2 polypeptide (II) of (I), a fusion polypeptide
CC      (III) of (I) and a method for modulating (M1) the physiology or
CC      development of a cell or tissue culture cells comprising contacting the
CC      cell with an agonist or antagonist of a mammalian DCRS2. (M1) is useful
CC      for modulating the physiology or development of a cell or tissue culture
CC      cells. (I)-(III) are useful for diagnosing or treating immunological
CC      disorders. The current sequence represents the nucleotide sequence of
XX      DNAX cytokine receptor subunit 2 (DCRS2).

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Sequence 1155 BP; 387 A; 233 C; 223 G; 312 T; 0 U; 0 Other;

Alignment Scores:

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US-10-667-289-2 (1-629) x AD265011 (1-1155)

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Qy      61  ProArgIleLeuHisPheTyrIleAsnGlyIleValGlnIlePheGlnIleThrArgIle 80
Db      181  CCAAGGAACCTCATTTTATTAATAAATGGCATCAAGAAAGATTTCAATCATCAAGGATT 240
Qy      81  AsnIleThrThrAlaArgLeuTrpTyrIleAsnPheLeuGluProHisIleSerMetTyr 100
Db      241  AATTAACAACACAGCTGGCTTGTGTATTAATACTTTCTGGAACCAATGCTTCTATGTAC 300
Qy      101  CysThrAlaGluCysProIleHisPheGlnIleLeuIleCysGlyIleValAspIleSer 120
Db      301  TGCACGTGTAATGTCCAAACATTTTCAAGAACACTGATATGTGAAAGACATTTCT 360
Qy      121  SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
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Qy      141  AsnMetThrCysThrTrpAsnAla***LysLeuThrTyrIleAspThrIleValIle 160
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Qy      161  HisValIleSerLeuGlnIleThrGlnIleGlnIleThrIleuThrSerSerTyrIleAsn 180
Db      481  CATGTGAAGATTTAAGACAGAAAGACCAAGATATCTCACTCAAGCTATATTAAC 540
Qy      181  IleSerThrAspSerLeuGlnIleGlyIleValTyrIleValIleTrpValIleAlaAsn 200
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Email: csgabes-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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DB      353  TGAACAGTCTTAATATGTTATGCCATGATTAACAGATTAAGAAATCTTCATCCCA 412
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VERSION      BP282008.1 GI:52195740
KEYWORDS      EST.
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  Mizushima-Sugano,J., Nakai,K. and Sugano,S.
  Sequence comparison of human and mouse genes reveals a homologous
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  Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL      PUBMED
PUBMED      15342556
COMMENT      Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Tel: 81-3-5449-5343
  Fax: 81-3-5449-5416
  Email: ysuzuki@igc.jp.

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US-10-667-289-2 (1-629) x BP282008 (1-583)

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 QY 284 UGUlProAsnIlelystTyValPheGlnValArgCysGlnGluThrGlyValysArgTyr 304
 Db 138 GAGAGCCAAACATTAAGTACGATTTTCAAGTACAGATGTCAGAAACAGGCAAAAGGTACTG 197
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 Db 198 GCAACCTTGAGTTACCGTGGTTTTTTCATTAACCACTGAAACAGTTCCTCCAGGTCAATC 257
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 QY 344 YHISleuThSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMetIleValPheAl 364
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 754)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaabs-rc@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LCM972 row: 9 column: 21
 High quality sequence stop: 650.
 Location/Qualifiers
 1..754
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="4101164"
 /issue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_54"

FEATURES

SOURCE

1..754
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="4101164"
 /issue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_54"

/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccgcgcgc); Site 2: SfiI
 (ggccatcagcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGCCATTAATGCGC-3' and
 3' adaptor sequence:
 5'-ATCTAGAGCCGACGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
414e-86	754	189	14	12	11	4
Score:	857.00					
Percent Similarity:	91.9%					
Best Local Similarity:	85.5%					
Query Match:	25.8%					

US-10-667-289-2 (1-629) x BF210400 (1-754)

QY 265 TTPAsn-VallyeGluPheAspThrAspPheThrTyValGlnGlnSergluPheTyLe 284
 Db 78 TGAACCTGTTAAAGAAATTGACACCAATTTTACATATGTGCAACAGTCAGATTTCTACTT 137
 QY 284 UGUlProAsnIlelystTyValPheGlnValArgCysGlnGluThrGlyValysArgTyr 304
 Db 138 GAGAGCCAAACATTAAGTACGATTTTCAAGTACAGATGTCAGAAACAGGCAAAAGGTACTG 197
 QY 304 PGIInProTyrSergSerpPhePheHISlystThProGluThrValProGlnValThrse 324
 Db 198 GCAACCTTGAGTTACCGTGGTTTTTTCATTAACCACTGAAACAGTTCCTCCAGGTCAATC 257
 QY 324 rTySalAphGlnHisAspThrTTPAsnSerglyLeuThrValAlaSerIleSerrhgI 344
 Db 258 AAAAGCATTCACATGACATGCAATTCGGCTACAGTTCTCCATCTCTACAGG 317
 QY 344 YHISleuThSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMetIleValPheAl 364
 Db 318 GCACCTTACTTCTGACAAACAGAGACATTTGACCTTTTATGGGAATGATCGCTTTTGC 377
 QY 364 aValMetLeuSerIleLeuSerrleuIleGlyIlePheAsnArgSerPheArgThrglyI 384
 Db 378 TGTATGTGTCAATTCCTTTCTTGATGGATATTTAAACAGATCATTCGAGT-GGAT 436
 QY 384 eLyAspArgIleLeuLeuLeuIleProlystRLeuTyrgIuAspIleProAsnMetly 404
 Db 437 TAAAGAAGATCTTATTTGTTAAACCAAGTGGTT-TATGAAATATCTTAATATGAA 495
 QY 404 SAASerAsnValVallySweLeuGlnGluAsnSergIleuLeuMetAsnAsnSergse 424
 Db 496 AAACAGCAATGTTGTGAAATGCTACAGAAATAGCAACTTATGAAATATATTCAG 555
 QY 424 rGluGlnValLeuTyValAspProMetIleThrgluIleGlnIlePheIleProG 444
 Db 556 TGAGCAGTCTCATATATGTATGCCATGATTAACAGAAAT-AAAGAAATCTTCATC--CA 611
 QY 444 UHISlyPProThAspTyTylySlyGluAsnThrglyProLeuGluThrArgAspTyPr 464
 Db 612 GAACAAAGCTACAGATCTACAGAAAGG-AATACAGACACCTGGGAC--AGAGAAAT-CC 666
 QY 464 OGInAsnSerrleuPheAspAsnThrThValValTyIleProAspLeuAsnThrglyTy 484
 Db 667 GGAAGAT---TGGTATTCGAATACTACAGGTGTTTCTG-----ATTCAACTGGTT 717
 QY 484 r 484
 Db 718 T 718

RESULT 4

BF209716 820 bp mRNA linear EST 06-NOV-2000
 LOCUS 601874259F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4098831 5',
 DEFINITION mRNA sequence.
 ACCESSION BF209716
 VERSION BF209716.1 GI:11103302
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 820)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM966 row: f column: 16
 High quality sequence stop: 608.
 Location/Qualifiers
 1..820
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4098831"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_54"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI
 (ggccatcagcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3' and
 3' adaptor sequence:
 5'-ATTGAGGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,566-83 Length: 820
 Score: 833.00 Matches: 182
 Percent Similarity: 89.84 Conservative: 3
 Best Local Similarity: 88.34 Mismatches: 14
 Query Match: 25.04 Indels: 8
 DB: 7 Gaps: 0
 US-10-667-289-2 (1-629) x BF209716 (1-820)
 Oy 431 AaPProMeTieTherGluLeuGluLeuPheHeleProGluNiSlySProThAspTy 450
 Db 1 GATCCCATGATTACGAGATAAAGAAATCTTCATCCGAAACCAAGCTCAGACTAC 60
 Oy 451 LysLysGluAanThngLyProLeuGluThrTrAspTyTyrProGlnAseSerLeuPheAsp 470
 Db 61 AAGAGAGGAATACAGATCCCTGGAGCAAGAGACTACCCGCAAAATCTGCTATTGCAC 120
 Oy 471 AaThrThValValTyTLeProAsPheAanThngLyTyLysProGlnLleSerAan 490
 Db 121 AATCTACAGTTGTATATTCTCGATTCTCAACACTGATTAACCCCAATTTCAAT 180
 Oy 491 PheLeuProGluGlySerHisLeuSerAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 510

Db 181 TTTCGCTTAGGAGGAGCCATCTCAGCAATTAATGAATTAATCTTCTTAACATT-AAA 239
 Oy 511 ProProValAaSerLeuAaSerGlyAaAaAaProAaGluGluTyHisProAaPhe 530
 Db 240 CACCAATTATATCTTAACTAGCTCAGAAATATATCCGAGTTTACAAAGCATCTTAATTG 299
 Oy 531 AlaPheSerValSerSerValAaSerLeuSerAaAaThrLlePheLeuGlyGluLeuSer 550
 Db 300 GCTTTCTGTTTCAAAAGTGTGAATTCCTAAGCAACACAAATATTTCTGTGAGAAATTAGC 359
 Oy 551 LeuLleLeuAaAaAaGluGlyGlySerSerProAspLle-GlnAaSerValGluGluGlu 570
 Db 360 CTATATTAATTAATCAAGAGAAATCAAGTCTCCGACATTAACAAATCACTAAGAGAGA 419
 Oy 570 UThrThMetLeu-LeuGluAaAaAaSerProSerGluThrLleProGluGlnThrLeuL 590
 Db 420 AACCAATGCTTTGTGAAATATGATTCACCCAGTGAATTCGAAACCAAGACTGC 479
 Oy 590 eUpProAaGluPhe-ValSerCys-LeuGlyLleValAaAaGlu-GluLeuProSerLleA 609
 Db 480 TTCTGATGATATTGGTCTCTGTTTGGGATTCGTGAATGAAGAGAGTGGCATCTATTA 539
 Oy 609 eThrTyTyrPheProGln-AaLle-LeuGluSerHisPheAaAaArgLleSerLeuL 628
 Db 540 ATATTATTTTCCACAAATATTTGTGAAAGCCACTTCATTAAGATTTCACCTCTGGG 599
 Oy 628 uLys 629
 Db 600 CAA 603
 RESULT 5
 BF238439 917 bp mRNA linear EST 14-NOV-2000
 LOCUS 601904735F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132593 5',
 DEFINITION mRNA sequence.
 ACCESSION BF238439
 VERSION BF238439.1 GI:1152359
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 917)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM1032 row: e column: 10
 High quality sequence stop: 575.
 Location/Qualifiers
 1..917
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4132593"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_54"
 /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI
 (ggccatcagcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3' and

3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Alignment Scores:

Pred. No.:	2,866-82	Length:	917
Score:	824.50	Matches:	185
Percent Similarity:	88.8%	Conservative:	6
Best Local Similarity:	86.0%	Mismatches:	18
Query Match:	24.8%	Indels:	10
DB:	7	Gaps:	1

US-10-667-289-2 (1-629) x BF238439 (1-917)

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Qy 265 TTPAen-VallysGluPheAepThrAanPheThrTyValGInGInSerGluPheTyLe 284
    |||||
Db 78 TGGAACTGTAAAGAAATTTGACCAATTTTACATATGTGACACAGTCAGAAATCTACTT 137

Qy 284 uGluProAanIleTyValPheGInValArgCyGInGInThrgIlyTyAArgTyTr 304
    |||||
Db 138 GGAGCCAAACATTAAGTACGTATTTCAAGTACAGATGTCAGAAACAGGCAAAAGTACTG 197

Qy 304 pGInProTTPSerSerProPhePheHIslyTyThProGInThrValProGInValThrs 324
    |||||
Db 198 GCACCTTGGAGTTCACCGTTCCTTTTCATMAAACATGAAACATTCCTCCAGTACATC 257

Qy 324 rLyValAPheGInHIsAepThrTPAenSer-GlyLeuThrValAlaserIleSerThrg 344
    |||||
Db 258 AAAAGCATTCACATGACATGACATGGAATTCGGGGCTTACAGTCTTCCATCTCTACG 317

Qy 344 lYHIsleuThrSerAspAanArgGlyAepIleGlyLeuLeuGlyMetIleValPhe 364
    |||||
Db 318 GGACCTTACTCTTGACACAGAGAGACATGGAATTTTATGGAATGATCGCTTTG 377

Qy 364 lAValMetLeuSerIleLeuSerIleGlyIlePheAanArgSerPheAArgThrgIy 384
    |||||
Db 378 CTGTTATGTGTCAATCTTCTTTCATGAGGAGATTTTACAGATTCATTCGAACCTGGGA 437

Qy 384 lelysArgArgIleLeuLeuIleProlystRpleuTyGluAapIleProAanMet 404
    |||||
Db 438 TTACAGAGAGATCTTATG-TTAAATACCAAGTGGCT-TATGAAATATTTCTTAATAGA 495

Qy 404 ysaenSerAanValIlyMetLeuGInGInAanSerGluLeuMetAanAanSers 424
    |||||
Db 496 AAAACACCAATGTTGTGAAAAATGCTACGAAAAATAGGAATTAATAATATCCCA 555

Qy 424 er-GluGInValIleuTyValAapProMetIleThrgIleIle-LysGluIlePheIlepr 443
    |||||
Db 556 GTTGAGACAGGTCTATATGTTGATCNCAATGATTAACGAGATACACAGAAATTCATCC 615

Qy 443 oGluHIslyerProThrAepTyTylyGluAanThrcIyProleuGInThrrArgAepTy 463
    |||||
Db 616 AGAATAA-AAAGCTACAGCTACAGAAAGGAGCTA-CAGGACCTGGGAAAGAGAGA----- 668

Qy 463 rProGInAanSerLeuPheAanThrThValVal 475
    |||||
Db 669 -TAACCGAAATCGCTATTGAAAAATACACGTGTGA 704
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RESULT 6
BF238869 823 bp mRNA linear EST 14-NOV-2000
LOCUS 60190492P1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132295 5',
DEFINITION mRNA sequence.
ACCESSION BF238869
VERSION BF238869.1 GI:11152790
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 823)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LICM1031 row: h column: 24
High quality sequence stop: 584.

FEATURES

source

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1. .823
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4132295"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH MGC 54"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccgtcgcc); Site 2: SfiI
(ggcacatcagcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
```

ORIGIN

Alignment Scores:

Pred. No.:	7,096-79	Length:	823
Score:	794.00	Matches:	190
Percent Similarity:	69.1%	Conservative:	16
Best Local Similarity:	63.8%	Mismatches:	25
Query Match:	23.9%	Indels:	72
DB:	7	Gaps:	4

US-10-667-289-2 (1-629) x BF238869 (1-823)

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Qy 265 TTPAen-VallysGluPheAepThrAanPheThrTyValGInGInSerGluPheTyLe 284
    |||||
Db 75 TGGAACTGTAAAGAAATTTTACCAATTTTACATATGTGACACAGTCAGAAATCTACTT 134

Qy 284 uGluProAanIleTyValPheGInValArgCyGInGInThrgIlyTyAArgTyTr 304
    |||||
Db 135 GGAGCCAAACATTAAGTACGTATTTCAAGTACAGATGTCAGAAACAGGCAAAAGTACT 194

Qy 304 rGInProTTPSerSerProPhePheHIslyTyThProGInThrValProGInValThrs 324
    |||||
Db 195 GGAGCTTGGAGTTCACCGTTCCTTTTCATMAAACATGAAACATTCCTCCAGTACAT 254

Qy 324 erLyValAPheGInHIsAepThrTPAenSerGlyLeuThrValAlaserIleSerThrg 344
    |||||
Db 255 CAAAGATTCACATGACATGACATGGAATTCGGGCTTACAGTTCCTCTACAG 314

Qy 344 lYHIsleuThrSerAspAanArgGlyAepIleGlyLeuLeu-LeuGlyMetIleValPhe 363
    |||||
Db 315 GGACCTTACTCTTGACACAGAGAGACATGGAATTTTATGGAATGATCGCTTT 374

Qy 364 lAValMetLeuSerIleLeuSerIleGlyIlePheAanArgSerPheAArgThrgIy 383
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ACCESSION CD708943
 VERSION GI:32239573
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 602)
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)
 COMMENT Contact: Yixun Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510660, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /isue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Alignment Scores:

Pred. No.:	8,996-75	Length:	602
Score:	756.00	Matches:	135
Percent Similarity:	99.3%	Conservative:	0
Best Local Similarity:	99.3%	Mismatches:	1
Query Match:	22.7%	Indels:	0
DB:	5	Gaps:	0

US-10-667-289-2 (1-629) x CD708943 (1-602)

QY 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
 Db 194 ATGATCATGCTCACTATTCATATGAGATCGAGTATATACCCCTTTCATACCTTCACTG 253

QY 21 CyHisGlyGlyIleThrAsnIleAsnCySerGlyHisIleTrpValIleGluProAlaThr 40
 Db 254 TGTCAATGAGAGAAATTCAAAATATTAATGCTGCGCACATCTGGTAGAACACGACCA 313

QY 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLeuAsnCysGln 60
 Db 314 ATTTTAAAGATGGTATGAATATCTATATATGCGAAGACGAATTAAGAACTGCGCA 373

QY 61 ProArgIleLeuHisPheTyrIleAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80
 Db 374 CCAAGGAAATCTCTTTTAAATAATGCGATCAAAAGAAATTTCAATACAGAGATT 433

QY 81 AsnIleThrThrAlaArgLeuTyrIleAsnIleLeuGluProHisAlaSerMetTyr 100
 Db 434 AATTAACAACAGCTCGCTTGTGTATAAAACTTTCGGAACACATGCTTATATGATAC 493

QY 101 CysThrIleAlaGluCysProIleHisPheGlnIleThrLeuIleCysGlyIleAspIleSer 120
 Db 494 TGCATGCTGAATGCTCCAAACATTTTCAAGAGACACTGATATGTGAAAAAGACATTTCT 553

QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyr 136
 Db 554 TCTGGATATCCGCGACGATATTCCTGATGAAGTAACCTGTGCAATTAT 601

RESULT 9
 CC496590 825 bp DNA linear GSS 17-JUN-2003
 LOCUS CC496590
 DEFINITION CH240_332J15.TARBAC132 CHORI-240 Bos taurus genomic clone

CH240_332J15, genomic survey sequence.
 ACCESSION CC496590
 VERSION GI:31811154
 KEYWORDS GSS.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 825)
 AUTHORS Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhakar, A.-L., Teal, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B.P. and Teliam, R.
 TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 JOURNAL Unpublished (2003)
 COMMENT Other GSSs: CH240_332J15..T7
 Contact: Rob Holt

Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccsc.ca
 Emails are derived from the bovine BAC library CHORI-240
 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
 Plate: 332 row: J column: 15
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 1..825
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="b:reel: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_332J15"
 /sex="male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site 1: MboI, Site 2: MboI; Hereford bull 1/1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:

Pred. No.:	5,696-69	Length:	825
Score:	707.00	Matches:	141
Percent Similarity:	83.8%	Conservative:	24
Best Local Similarity:	71.6%	Mismatches:	30
Query Match:	21.3%	Indels:	2
DB:	12	Gaps:	2

US-10-667-289-2 (1-629) x CC496590 (1-825)

QY 434 IleThrGluIleLeuGluIlePheIleProGluHisIleProThrAspTyrIleGlyGlu 453
 Db 3 ATTAACAGATA--GAAATCATTTCTCCGAGAGAAACCAATGGCTCAAGAAAGAA 59

QY 454 ---AsnThrGlyProLeuGluThrArgAspTyrProGluAsnSerLeuPheAspThr 472
 Db 60 AACATACAGAGAGCTCGAG 119

QY 473 ThrValValTyrIleProAspLeuAsnThrGlyTyrIleProGluIleSerAsnIleLeu 492
 Db 120 ACAGTGTATATTCCTGATCTCAACACTGGGTATTAACCCAGATTTCAGATTTCCTC 179

DB: 7 Gaps: 0

US-10-667-289-2 (1-629) x BF185326 (1-842)

Qy 479 Aspleuanshrnglytyrlyseproglinleaseraphneleuproglyserhileu 498
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 Db 1 GATCTCAACCTGGATATTAACCCCAATTTCTGCTGAGGAGGACCATCTC 60

Qy 499 SerAsnaansngliuierhserleuthleuysprovalaasSerleuaspser 518
 |||||
 Db 61 AGCATATATATGAATTAATCTCTTAACCTTAACACAGTGAATCTTACTCA 120

Qy 519 GlyAsnaansprogluengluysheleproasnahealapheserValserSerValasn 538
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 Db 121 GGAATATATCCAGGTACAAAGCATCTAA-TTTCTTTTCTGTTTCAAGTGAAT 179

Qy 539 SerleuSeranhrillepheleuglyluenseerleuleuansngliuGluCys 558
 |||||
 Db 180 TCACTAAGCAACACATATTTCT-GGAGAAATTAGCTCATATTAATCAAGGAAATGC 238

Qy 559 SerSerProaspilleglaasSerValgluGluGluThrMetLeuLeuGluAsnaasp 578
 |||||
 Db 239 AGTTCTCTGACACACAAAATCTAGTAGAGAGAAACCAACATGCT-TTGAAAAATGAT 297

Qy 579 SerProsergluthrilleprogluGluThrleuLeuProaspGluPheValSerCysleu 598
 |||||
 Db 298 TCACCCAGTGAATATTCACAGAACACCTGCTCTCATGTAAT-GTCTCTCTGTG- 355

Qy 599 GlyleValansngluLeuProSerilleasnthrTyrrPheProGluAsnilleleuGlu 618
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 Db 356 GGAATCGTAATGAGGATTCGCACTATTAATCTTAATTTCCACAAAATAT-TTGAAA 414

Qy 619 SerHisPheAsnaArgilleSerleuLeuGluys 629
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 Db 415 AGCCACTTCATAGATTCACTTGGAAAAG 447

RESULT 13
 BF185326 430 bp mRNA linear EST 31-OCT-2000
 LOCUS 601844139F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064840 5',
 DEFINITION mRNA sequence.
 ACCESSION BF185326
 VERSION BF185326.1 GI:11063769
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 Qy 1 (bases 1 to 430)
 Db NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: ggaube-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LHC699 row: n column: 09
 High quality sequence stop: 388.
 Location/Qualifiers
 1. 430
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 /clone="IMAGE:4064840"
 /tissue_type="from chronic myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_54"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Best Local Similarity:	451.00	430	100	2	6	39	1
Best Local Similarity:	69.94						
Query Match:	68.54						
DB:	13.64						
US-10-667-289-2 (1-629) x BF185326 (1-430)							

/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctcgcc); Site 2: SfiI
 (ggcctatggcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
 3' adaptor sequence:
 5'-ATTCTAGAGCCAGGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

Qy 265 TTPAsn-VallyeGluPheasPhrhnaphethrTyrrValGlnGlnSerGluPheTyrrle 284
 |||||
 Db 78 TGAAACGTGTAAGAAATTTGACACCAATTTTACATATGTGCAACAGTCAGAAATTTCACTT 137

Qy 284 UGUProAsnilleuetyrValPheGluValArgCysGluGluThrGly-LysArgTyrr 304
 |||||
 Db 138 GGAGCCAAACATTAAGTACGTAATTTCAAGTGAAATGTCAGAAACAGGAAAGGATCT 197

Qy 304 TpolPro-TrypSerSer-ProphepheileuetyrThrProGluThrValProGluValTh 323
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 Db 198 GGACGCTTGAAGATTGACACCGCGTTTTCATAAACACCTGAAACAGTTCCCGAGGTCAC 257

Qy 323 rSerlyValaPheGluHisaphThrTrpAsnSerGlyLeuThValaSerilleSerTh 343
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 Db 258 ATCAAAAGCAATTCACATGACATGAGAAATTCGAGCTAACAGTTCCTTCATCTCTAC 317

Qy 343 rGlyHisleuThSerAsnaArgGlyAspilleGlyLeuLeuGluyleuValPh 363
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 Db 318 AGGGCACCTTACTTCT----- 333

Qy 363 eaValaMetleuSerilleuSerleuileGlyllePheAsnaArgSerPheArgThrgl 383
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 Db 334 -----GG 335

Qy 383 yllelyAsArgGlylleuLeuLeuileProlyeTTPleuTyrrGluAspilleProasme 403
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 Db 336 ATT-AAAGAGAGATCTTATGTTAAATCCAAAGTGCTTTATGAAGATATTCCTACATC 394

Qy 403 LlyAsnaSer 406
 |||||
 Db 395 TGAAAAGACA 404

RESULT 14
 AO699233 569 bp DNA linear GSS 06-JUL-1999
 LOCUS HS_5565_A1 H02 T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=1141 Col=3 Row=O, genomic survey sequence.
 ACCESSION AO699233
 VERSION AO699233.1 GI:5389481
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 Qy 1 (bases 1 to 569)
 Db NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Kellera,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

QY	584	11eProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGlu	603
Db	145	ATTCCAGAACAGACCCCTGCTCTCGATGAATTTGTCTCTCTGTTGGAAATCGTGAATGAG	204
QY	604	GluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHisPheAsnArg	623
Db	205	GAGTTGCCATCTATTAACTTATTTCACAAAATATTGGAAAGCCACTTCATATAG	264
QY	624	11eSerLeuLeuGluLys	629
Db	265	ATTCACTCTTGGAAAAG	282

Search completed: October 14, 2006, 16:52:19
Job time : 7930 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 14, 2006, 14:25:09 ; Search time 9842 Seconds
(without alignments)
6130.298 Million cell updates/sec

Title: US-10-667-289-2
Perfect score: 3326
Sequence: 1 MNXVTRIQMDAVIALYILFSM.....TYPNPILSHFNRIILK 629

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSMB.spool/US10667289/runat_13102006_11532_24363/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEADING=580 -MINLEN=0 -MAXLEN=200000000 -HOST=abs602h
-USER=US10667289.QCGN_1.1.6194@runat_13102006_11532_24363 -NCPU=6 -ICPU=3
-NO_MMAPP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV.TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_pat:.*
3: gb_ph:.*
4: gb_pl:.*
5: gb_dr:.*
6: gb_ro:.*
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8: gb_sy:.*
9: gb_un:.*
10: gb_vl:.*
11: gb_ov:.*
12: gb_ncg:.*
13: gb_in:.*
14: gb_cm:.*
15: gb_ba:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3324	99.9	2826	5	AF461422 Homo sapi
2	3324	99.9	2859	2	C0878371 Sequence
3	3324	99.9	2859	2	CS110317 Sequence

4	3324	99.9	2859	2	AR561607	AR561607 Sequence
5	3324	99.9	2859	2	AX338549	AX338549 Sequence
6	3314	99.6	1890	2	AX467350	AX467350 Sequence
7	3314	99.6	1910	2	BD013245	BD013245 Novel hem
8	3314	99.6	2830	2	AX467349	AX467349 Sequence
9	3292	99.0	2123	2	BD013243	BD013243 Novel hem
10	3123	93.9	1779	5	AY937250	AY937250 Homo sapi
11	2952	88.8	1698	5	AX467352	AX467352 Sequence
12	2889	86.9	1676	5	AY937253	AY937253 Homo sapi
13	2889	86.9	1676	5	AY937254	AY937254 Homo sapi
14	2785	83.7	1618	5	AY937251	AY937251 Homo sapi
15	2785	83.7	1618	5	AY937252	AY937252 Homo sapi
16	2764	83.1	1609	5	AY937255	AY937255 Homo sapi
17	2747	82.6	1887	2	AX338551	AX338551 Sequence
18	2284.5	68.7	2488	6	AF461423	AF461423 Mus muscu
19	2280.5	68.6	1935	2	AX467359	AX467359 Sequence
20	2192	65.9	1301	2	BD013244	BD013244 Novel hem
21	2115	65.4	1479	2	BD013242	BD013242 Novel hem
22	2039	61.3	1155	2	AX054989	AX054989 Sequence
23	1902	57.2	1324	5	BC016829	BC016829 Homo sapi
24	1868	56.2	1071	2	AX467354	AX467354 Sequence
25	1747	52.5	1152	2	AX054991	AX054991 Sequence
26	1695	51.0	1784	2	BD013241	BD013241 Novel hem
27	1511	45.4	1532	5	BC040720	BC040720 Homo sapi
28	1122	33.7	122289	5	AL389925	AL389925 Human DNA
29	709	21.3	220412	12	AC167151	AC167151 Bos tauru
30	659	19.8	219288	12	AC111912	AC111912 Rattus no
31	659	19.8	235198	12	AC106222	AC106222 Rattus no
32	659	19.8	236635	12	AC126525	AC126525 Rattus no
33	620	18.6	110000	12	AY657029	AY657029 Contination (4 of
34	620	18.6	181390	6	AC159129	AC159129 Mus muscu
35	620	18.6	216956	6	AC124758	AC124758 Mus muscu
36	552	16.6	114713	5	HS077631	AL109843 Human DNA
37	550	16.5	439	2	C0745744	C0745744 Sequence
38	456.5	13.7	276459	12	AC110385	AC110385 Rattus no
39	442	13.3	99950	12	AY657029	AY657029 Contination (5 of
40	339	10.2	239653	12	AC122650	AC122650 Rattus no
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42	283	8.5	966	11	CR386407	CR386407 Gallus ga
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44	276	8.3	2577	11	AJ374496	AJ374496 Gallus ga
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ALIGNMENTS

RESULT 1	AF461422	2826 bp	mRNA	linear	PRI 29-MAY-2002
LOCUS	Homo sapiens interleukin-23 receptor (IL-23R)				complete cds.
DEFINITION	AF461422				
ACCESSION	AF461422.1	GI:21239251			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	Homo sapiens (human)				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homidae; Homo.				
	1 (bases 1 to 2826)				
REFERENCE	Parham,C., Chirica,M., Timans,J., Valseberg,E., Travis,M.,				
AUTHORS	Cheung,J., Pflanz,S., Zhang,R., Singh,K.P., Vega,F., To,W.,				
	Wagner,J., O'Farrell,A.-M., McClanahan,T., Zurawski,S., Hannum,C.,				
	Gorman,D., Rennick,D.M., Kastelein,R.A., de Waal Malefyt,R. and				
	Moore,K.W.				
TITLE	A receptor for the heterodimeric cytokine IL-23 is composed of				
	IL-12Rbeta1 and a novel cytokine receptor subunit, IL-23R				
JOURNAL	J. Immunol. 168 (11), 5699-5708 (2002)				
PUBMED	12023369				
REFERENCE	2 (bases 1 to 2826)				
AUTHORS	Parham,C., Chirica,M., Timans,J., Valseberg,E., Travis,M.,				
	Cheung,J., Pflanz,S., Zhang,R., Singh,K.P., Vega,F., To,W.,				
	Wagner,J., O'Farrell,A.-M., McClanahan,T., Zurawski,S., Hannum,C.,				
	Gorman,D., Rennick,D.M., Kastelein,R.A., de Waal Malefyt,R. and				

TITLE Moore,K.W.
Direct Submission
JOURNAL Submitted (19-DEC-2001) Immunology, DNA Research, 901 California Ave., Palo Alto, CA 94304, USA

FEATURES
Source location/Qualifiers
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86..1975
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SLLEK"

ORIGIN

Alignment Scores:

Prod. No.: 0 Length: 2826
Score: 3324.00 Matches: 627
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 2
Query Match: 99.9% Indels: 0
DB: 5 Gaps: 0

US-10-667-289-2 (1-629) x AF461422 (1-2826)

QY 1 MetAsn**ValThrIleGIINTPASPAlaValIleAlaLeuTYrIleLeuPheSerTyr 20
DB 86 ATGAAATAGGCTCACTATTCAATGGATGCACTAATACCCCTTACATACCTTCACTG 145
QY 21 CyHISGLYGLYIleThraenIleasnCySerGlyYHISileTyrValGIuProAlaThr 40
DB 146 TGTCAATGGAAGATTACAAATATTAATCTGCTGGCCACATCTGGGTAGAACCAAGCA 205
QY 41 IlePheIleMetGlyMetAsnIleSerIleTyrCySGlnAlaAlaIleIleYasnCySGln 60
DB 206 ATTTTAAAGATGGGTATGAATATCTCTATATATTGGCCAAACAGCAATTAAGAACTGGCAA 265
QY 61 ProArgGlySerLeuHISpHeTYrLYASnGLYIleIleSGluARophGlnIleThraSYIle 80
DB 266 CCAAGGAACCTCTCTTTTATTAATAATGGCATCAAAAGAAATTTCAAATCACAAGGATT 325
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DB 326 AATTAACAACACAGCTGGCTTGGTATTAATAAATCTTCTGGAACCACTGCTTCAATGAC 385
QY 101 CysThrIlaGluCYSPOLYSHISpHeGlnGluThrIleuIleCYSGLYLYSAspIleSer 120
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QY 121 SerGlyTyrProProAspIleProAspGluValThrcysValIleTYrGluTYrSerGly 140
DB 446 TCTGGATATCCGGCCAGATATCTCGATGAAGTAACTGCTGCTATTATGAATATTCAGGC 505
QY 141 AsnMetThrcysThrTyrAsnAla**LYSLeuThrTYrIleAspThrLYSValVal 160

DB 506 AACATACCTTGACCTGGAAATGCTGGAGAGCTCACCTACATATGACCAAAATATCTGGTA 565
QY 161 HISValIleSerLeuGIuThrGIuGIuGIuGIuGIuGIuTYrIleThrSerSerTYrIleAsn 180
DB 566 CATGTAAAGAGTTTAAAGACAGAAAGAGCAAGATATCTCACTCAACGTATATTAAC 625
QY 181 IleSerThrAspSerLeuGlnGlyLYSLYSValIleTyrValIleAlaAsn 200
DB 626 ATCTCCAGTATTCATTATCAAGGTGGCAAGAGTACTTGTTGGGTCCAGACAGCAAC 685
QY 201 AlaLeuGlyMetGluGluSerLYSGlnLeuGlnIleHISLeuAspAspIleValIlePro 220
DB 686 GCACGTAGGATGGAAGACAAACCAACGCAAAATTCACCTGATGATATGATGATACCT 745
QY 221 SerAlaAlaValIleSerArgIaGluThrIleAsnAlaThrValProThrThrIleIle 240
DB 746 TCTGACGCGCTCATTTCCAGGCGCTGAGACTATTAATGCTACAGTCCCAAGACATAT 805
QY 241 TYTTPASPserGlnThrThrIleGluLYSValSerCYSGluMetArgTYrLYSAlaThr 260
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QY 261 ThrAsnGlnThrTyrAsnValLYSGluPhelAspThrAsnPhetThrTYrValGlnGlnSer 280
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DB 926 GAATTTCTTGGAGCCCAACATTAAAGTACGATTTCAAGTGAAGATGTCAGAAACAGGC 985
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QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
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QY 381 ArgThrGlyIleLYSArgArgIleLeuLeuLeuIleProLYSTyrLeuTYrGluAspIle 400
DB 1226 CGAACTGGGATTAAGAAAGAGATCTTATGTTAATCCAAAGTGGCTTTATGAAATATT 1285
QY 401 ProAsnMetLYSAsnSerAsnValValLYSMetLeuGlnIuAsnSerGIuLeuMetAsn 420
DB 1286 CTTAATATGAAGAAACGCAATGTGTGAATAATGCTACAGAAATATGTAACTTATGAAT 1345
QY 421 AsnAsnSerSerGlnIuValLeuTYrValAspProMetIleThrGluIleLYSGluIle 440
DB 1346 AATTAATTCAGAGAGAGGCTCTATATGTTGATCCCATGATTACAGATTAATAAGAAATC 1405
QY 441 PheIleProGluHISLYSProThrAspTYrLYSGLYAsnThrGlyProLeuGluThr 460
DB 1406 TTCATCCAGAACACAGGCTTACAGACTACAGAAAGAAATACAGAGCCCTCGAGAAC 1465
QY 461 ArgAspTYrProGIuAsnSerLeuPheAspAsnThrThrValValTYrIleProAspLeu 480
DB 1466 AGAGACTACCCGCAAACTCGCTATTGCAATATCTACAGTTGTTATATATCTGATCTC 1525
QY 481 AsnThrGlyTYrLYSProGlnIleSerAsnPhelLeuProGluGlySerHISLeuSerAsn 500
DB 1526 AACACTGATATTAACCCCAATTTTCTGCTCGAGAGGAAGCCATCCACCAAT 1585
QY 501 AsnAsnGluIleThrSerLeuThrLeuLYSProProValAspSerLeuAspSerGlyAsn 520

Db 1586 AATATGAAATTAATCTTCTTAACCTTAACCAACAGTGTATCTTACAGCAAGAAAT 1645
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Qy 541 SerAsnThrIlePheLeuGlnGlyLeuSerLeuIleLeuAsnGlnGlyGlyCysSerSer 560
Db 1706 AGCAACACATATTTTCTTGAGAAATTAGCTCATATTAATACAGAGAAATGAGTTCT 1765
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Db 1766 CTGACATACAAACCTAGTAAAGAGAGAAACCAACATGCTTTTGAATAATTCACACC 1825
Qy 581 SerGlnThrIleProGlnGlnThrLeuLeuProAspGlnPheValSerCysLeuGlyIle 600
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Db 1886 GTGATACAGAGAGTTGCCATCTATTAATACCTATTTTCCACAAATATTTGGAAAGCCAC 1945
Qy 621 PheAsnArgIleSerLeuLeuGlnGlyLeu 629
Db 1946 TTCAATGAGATTCACTCTTGAAAG 1972

RESULT 2
CQ878371 2859 bp DNA linear PAT 04-OCT-2004
LOCUS CQ878371
DEFINITION Sequence 5 from Patent WO2004081190.
ACCESSION CQ878371
VERSION CQ878371.1 GI:53790924
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS Olt,M. and Mcclanahan,T.K.
TITLE Uses of 11-23 agonists and antagonists; related reagents
JOURNAL Patent: WO 2004081190-A 5 23-SEP-2004;
SCHERING CORPORATION (US)
FEATURES
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REFERENCE 1
AUTHORS Chirica,M., Kastelein,R.A., Moore,K.W. and Parham,C.L.
TITLE 11-23 and its receptor; related reagents and methods
JOURNAL Patent: WO 2005052157-A 1 09-JUN-2005;
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 ORGANISM Unknown.
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 AUTHORS Chirica, M., Kaelelein, R. A., Moore, K. W. and Parham, C. L.
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 Schering Corporation; Kenilworth, NJ
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 DB 1979 TTCATTAAGATTTCACTCTTGAAAAAG 2005

RESULT 5
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 DEFINITION Sequence 1 from Patent WO0185790.
 ACCESSION AX338549
 VERSION AX338549.1 GI:18128949
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE 1
 AUTHORS Chirica, M., Kastelein, R. A., Moore, K. W. and Parham, C. L.
 TITLE Mammalian receptor proteins; related reagents and methods
 JOURNAL Patent: WO 0185790-A 1 15-NOV-2001,
 SCHERING CORPORATION (US)
 FEATURES
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US-10-667-289-2 (1-629) x AK338549 (1-2859)

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AX467350

LOCUS AX467350 1890 bp DNA linear PAT 16-JUL-2002
 DEFINITION Sequence 20 from Patent WO0229060.
 ACCESSION AX467350
 VERSION AX467350.1 GI:21900587
 KEYWORDS
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE
 AUTHORS Cosman, D. J., Mosley, B. A., Bird, T. A., Dubose, R. F. and Wiley, S. R.
 TITLE Hematopoietin receptors hpr1 and hpr2
 JOURNAL Patent: WO 0229060-A 20 11-APR-2002;
 Immunex Corporation (US)
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DEFINITION Novel hemopoietin receptor protein, NR12.
ACCESSION BD013245
VERSION BD013245.1 GI:22093434
KEYWORDS WO 0123556-A/5.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1910)
AUTHORS Maeda,M. and Yaguchi,N.
TITLE Novel hemopoietin receptor protein, NR12
JOURNAL Patent: WO 0123556-A 5 05-APR-2001;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, ASATSUGU
MAEDA, NORIKO YAGUCHI
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PN WO 0123556-A/5
PD 05-APR-2001
PR 27-SEP-2000 WO 2000JP006654
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ACCESSION AX467349
VERSION AX467349.1 GI:21900586
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REFERENCE
  1 Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
    Hematopoietin receptors hpr1 and hpr2
    Patent: WO 0229060-A 19 11-APR-2002;
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 ACCESSION BD013243
 VERSION BD013243.1 GI:22093432
 KEYWORDS NO 0123556-A/3.
 SOURCE Homo sapiens (human)
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 1 (bases 1 to 2123)
 REFERENCE
 AUTHORS Maeda,M. and Yaguchi,N.
 TITLE Novel hemopoietin receptor protein, NR12

JOURNAL Patent: WO 0123556-A 3 05-APR-2001;
 CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, ASATSUGU
 MAEDA, NORIKO YAGUCHI
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 PN WO 0123556-A/3
 PD 05-APR-2001
 PR 27-SEP-2000 WO 2000/006654
 PR 27-SEP-1999 JP 99P 273358, 03-AUG-2000 JP 00P 240397 PI
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 PC C12N15/12, C12N1/21, C12N5/10, C07K14/715, C07K16/28, C12P21/02, PC
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ACCESSION      AY937250
VERSION      AY937250.1 GI:62870698
KEYWORDS
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Homnidae; Homo.
1 (bases 1 to 1779)
Zhang, X. Y., Zhang, H. J., Zhang, Y., Fu, Y. J., He, J., Zhu, L. P.,
Wang, S. H. and Liu, L.
Identification and expression analysis of alternatively applied
isoforms of human interleukin-23 receptor gene in normal lymphoid
cells and selected tumor cells
Immunogenetics 57 (12), 934-943 (2006)
16372191

JOURNAL
PUBMED
2 (bases 1 to 1779)
Zhang, X. -Y., Zhang, Y., Wang, S. -H. and Liu, L.
Direct Sublation
Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
Medical College, #5 Dong Dan San Tiao, Beijing 100005, China

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US-10-667-289-2 (1-629) x AY937250 (1-1779)

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 QY 357 LeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePhe 376
 Db 961 TTTATGGGAATGATCGCTTCTGCTTATATTTGTCATTTCTTTCTTGGATGGGATATTT 1020
 QY 377 AsnArgSerPheArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeu 396

Db 1021 AACAGATCATTCGGAACGCGGATTTAAAGAGAGATCTTGTTAAATACCAAGTGGCTT 1080
 QY 397 TyrGluAspIleProAsnMetLysAsnSerAsnValIleLysMetLeuGlnGluAsnSer 416
 Db 1081 TATGAAGATATTTCTTAATATGAAAAACACCAATGTTGTGAAAAATGCTACAGAAATATGT 1140
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 Db 1141 GAACCTATGAATATATATATCCAGTGAGAGGTCCTTATATGTTGATCCCATGATTACAGAG 1200
 QY 437 IleLysGluIlePheIleProGlnHisLysProThrAspTyrLysLysPheLeuThrGly 456
 Db 1201 ATTAAGAAATCTTCACTCCAGAACCAAGCCCTACAGCTACAGAAAGAGAAATACAGGA 1260
 QY 457 ProLeuGluThrArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValIleTyr 476
 Db 1261 CCCCTGAGACAGAGACTACCCGCAAACTGCTTATTTGACATATCTACAGTTGATAT 1320
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 Db 1321 ATTCCTGATCTCAACTGATATTAACCCAAATTTCAAAATTTCTGCTGAGGGAAGC 1380
 QY 497 HisLeuSerAsnAsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeu 516
 Db 1381 CATCTCAGCAATATATATGAATATCTCTTCAACCTTAACCTTAACACACAGTGTATCTTA 1440
 QY 517 AspSerGlyAsnAsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSer 536
 Db 1441 GACTCAGAAATATATCCAGGTACAAAGATCCTAATTTTGCTTTTGTTCAAGT 1500
 QY 537 ValAsnSerLeuSerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGly 556
 Db 1501 GTGAATTCATACAGCAACACAAATTTCTTGAGATTAAGCTCATATTAATTAACAAGA 1560
 QY 557 GluCysSerSerProAspIleGlnAsnSerValGluGluGluThrThrMetLeuGlu 576
 Db 1561 GAATGCAATTCCTCTGACATACAAACCTAGTAGAGAGAAACCACTGCTTTGGAA 1620
 QY 577 AsnAspSerProSerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSer 596
 Db 1621 AATGATTCACCCAGTAACTATTCAGAACACAGACCTGCTTCTTAATGAATTTGTCTCC 1680
 QY 597 CysLeuGlyIleValAsnGluLeuProSerIleAsnThrTyrPheProGlnAsnIle 616
 Db 1681 TGTTTGGGATCTGTGAATGAGAGTTGCCATCATTAATTAATTTTCCAGAAATATT 1740
 QY 617 LeuGluSerHisPheAsnArgIleSerLeuLeuGluLys 629
 Db 1741 TTGGAAGCCACTTCAATAGATTTCACTTGGAAAAAG 1779

RESULT 11
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 DEFINITION Sequence 22 from Patent WO0229060.
 AX467352
 ACCESSION AX467352
 VERSION AX467352.1 GI:21900588
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
 Hematopoietic receptors hprt and hprt2
 Patent: WO 0229060-A 22 11-APR-2002;
 ImmuneX Corporation (US)
 Location/Qualifiers
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ORIGIN

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US-10-667-289-2 (1-629) x AX467352 (1-1698)

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DB      121 ATTTTAAAGATGGGTATGAAATATCTGATATATTGGCAACAGCAATTAAGAACTGCCAA 180
QY      61 ProArgLysLeuHhIlePheTyrLysAenGlyIleLysGluArgPheGlnIleThrArgIle 80
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DB      181 CCAAGGAACTTCATTTTAAATAAATGCGATCAAGAAAGATTTCAAATCACAAAGATT 240
QY      81 AenLysThrThraAlaArgLeuTyrTyrLysAenPheLeuGluProHhIleSerMetTyr 100
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DB      241 AATTAACAAACAGCTGGCTTGGGTATTAATACTTTCTGAAACACATGCTTCTATGTAC 300
QY      101 CysThrAlaGluCyProLysHhIlePheGlnGluThrLeuIleCySerGlyLysAspIleSer 120
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DB      301 TGCACGCTGAAATGTCCTCAAAACATTTTCAAGAGACATGATATGTGAAAGACATTTCT 360
QY      121 SerGIyTyrProProAspIleProAspGluValIleThrCysValIleTyrGluTyrSerGIy 140
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QY      241 TyrTrpAspSerGlnThrThrIleGluLysValSerCySerGluMetArgTyrLysAlaThr 260
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DB      951 ----- 951
QY      341 IleSerThrGIyHhIleuThrSerAspAenArgGlyAspIleGIyLeuLeuLeuGIyMet 360
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QY      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGIyIlePheAenArgSerPhe 380
DB      951 ----- 951
QY      381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
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DB      1009 CCTAATATGAAAAACAGCAATGTGTGAAAAATGCTACAGAAAAATGTGCAACTTAAGAAAT 1068
QY      421 AenAenSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440
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DB      1189 AGAGACTTACCCGCAAACTCGCTATTCGACAAATACATCAAGTGTATATATTCCTGATCC 1248
QY      481 AenThrGIyTyrLysProGlnIleSerAenPheLeuProGluGIySerHhIleuSerAen 500
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DB      1249 AACACTGAATATTAACCCCAATTTCAATTTTCTGCTGAGAGAAAGCACTTCAGCAAT 1308
QY      501 AenAenGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGIyAen 520
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DB      1309 AATTAATGAATTAATCTCTTAAACACTTAACCAACCAAGTTGATTCCTTAACCTCAGGAAAT 1368
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DB      1369 AATCCAGGTTACAAAGATCTTAATTTTGCTTTTCTGTTTCAAGTGTGAATTCACATA 1428
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DB      1549 AGTGAATCAATTCCAAAACAGACCCCTGCTCGAAGAAATTTGCTCCGTGTTGGGAGATC 1608
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DB      1609 GTGAATGAGAGATGCACTATTAATCACTTATTTTCCACAAATATTTTGGAAACCCAC 1668
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RESULT 12

AY937253 1676 bp mRNA linear PRI 07-FEB-2006
 LOCUS
 DEFINITION Homo sapiens interleukin 23 receptor isoform 3 FI mRNA, partial
 cds alternatively spliced.
 ACCESSION AY937253
 VERSION AY937253.1 GI:62870704

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P., Wang,S.H. and Liu,L.
TITLE Identification and expression analysis of alternatively spliced isoforms of human interleukin-23 receptor gene in normal lymphoid cells and selected tumor cells
JOURNAL Immunogenetics 57 (12), 934-943 (2006)
PUBMED 16372191
REFERENCE 2 (bases 1 to 1676)
AUTHORS Zhang,X.Y., Zhang,Y., Zhang,H.-J., Wang,S.-H. and Liu,L.
TITLE Direct Submission
SUBMITTED (16-FEB-2005) Microbiology and Etiology, Peking Union Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
LOCATION/Qualifiers
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QY 57 LysAsnCysGlnProArgIleuHisPheTyrIleAsnGlyIleIleGluArgPheGln 76
DB 61 AAAAACTGCACCAAGCAAACTTCATTTTATTAATAATGCGATCAAGAAAGATTTCAA 120
QY 77 IleThrArgIleAsnIleSerThrAlaArgLeuTrpTyrIleAsnPheLeuGluProHis 96
DB 121 ATCCAGAGATTATTAATAACAACAGCTCGCTTTGGATTAATAAATTCCTCGAACCACAT 180
QY 97 AlasSerMetTyrCysThrAlaGluCysProIleHisPheGlnGluThrLeuIleCysGly 116
DB 181 GCTTCTATGATGACGACTGCTGAATGCTCCAAACATTTTCAAGAGACATGATATGGA 240
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RESULT 13
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LOCUS AY937254
DEFINITION Homo sapiens interleukin 23 receptor isoform 3 F3 mRNA, partial
cds, alternatively spliced.
ACCESSION AY937254
VERSION AY937254.1 GI:62870706
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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            Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P.,
            Wang,S.H. and Liu,L.
TITLE Identification and expression analysis of alternatively spliced
            isoforms of human interleukin-23 receptor gene in normal lymphoid
            cells and selected tumor cells
JOURNAL Immunogenetics 57 (12), 934-943 (2006)
PUBMED 16372191
REFERENCES
2 (bases 1 to 1676)
AUTHORS Zhang,X.-Y., Zhang,Y., Zhang,H.-J., Wang,S.-H. and Liu,L.
TITLE Direct Submision
SUBMITTED (16-FEB-2005) Microbiology and Etiology, Peking Union
            Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
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Score: 2889.00
Percent Similarity: 93.4%
Best Local Similarity: 93.4%
Query Match: 86.9%
DB: 5
Gaps: 1
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Db	936	-----	936
QY	377	AsnArgSerPheArgThrGlyIleValArgArgIleLeuLeuLeuIleProlySTPLeu	396
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QY	397	TyrGluAspIleProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSer	416
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QY	417	GluLeuMetAsnAsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGlu	436
Db	1038	GAACCTATGAAATATATATTCAGTGAGCAGTCTCTATATGTTGATCCCATGATTACAGAG	1097
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QY	457	ProLeuGluThrArgAspTyrProGluAsnSerIleuPheAsnThrThrValValTyr	476
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QY	477	IleProAspLeuAsnThrGlyTyrLysProGluIleSerAsnPheLeuProGluGlySer	496
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QY	557	GluCysSerSerProAspIleGlnAsnSerValGluGluGluThrMetLeuLeuGln	576
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QY	577	AsnAspSerProSerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSer	596
Db	1518	AATGATTCACCCAGGAACTTATTCAGAACAGACCTGCTTCTTGATGAAATTTGTCTCC	1577
QY	597	CysLeuGlyIleValAsnGluGluLeuProSerIleAsnThrTyrPheProGluAsnIle	616
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QY	617	LeuGluSerHisPheAsnArgIleSerLeuLeuGluLys	629
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DEFINITION			Homo sapiens interleukin 23 receptor isoform 2 fl mRNA, partial
ACCESSION	AY937251		cds, alternatively spliced.
VERSION	AY937251.1	GI:62870700	
KEYWORDS			
SOURCE			Homo sapiens (human)
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE	1 (bases 1 to 1618)		
AUTHORS	Zhang,X.Y., Zhang,H.J., Zhang,Y., Fu,Y.J., He,J., Zhu,L.P., Wang,S.H. and Liu,L.		
TITLE	Identification and expression analysis of alternatively spliced isoforms of human interleukin-23 receptor gene in normal lymphoid cells and selected tumor cells		
JOURNAL	Immunogenetics 57 (12), 934-943 (2006)		
PUBMED	16372191		
REFERENCE	2 (bases 1 to 1618)		
AUTHORS	Zhang,X.-Y., Zhang,Y., Wang,S.-H. and Liu,L.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union Medical College, #5 Dong Dan San Tiao, Beijing 100005, China		
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QY	57	LysAsnCysGlnProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGln	76
Db	61	AAGAATCGCCAAACAGAACTTCAATTTTATTAATAATGCGATCAAGAAAGATTCCA	120
QY	77	IleThrArgIleAsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHis	96
Db	121	ATCACAAGAGATTATTAACACACAGCTCGCTTGTATTAATAAATCTTTCGAAACACAT	180
QY	97	AlaSerMetTyrCysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGly	116
Db	181	GCTTCTATGTAAGTCTGCTGTAATGTCCAAACATTTTCAGAGACACATGATATGGA	240
QY	117	LysAspIleSerSerGlyTyrProProAspIleProAspGluValThrCysValIleTyr	136
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QY	137	GluTyrSerGlyAsnMetThrCysThrTyrPheAla**LysLeuThrTyrIleAspThr	156
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QY	157	LysTyrValValHisValLysSer-LeuGluThrGluGluGlnGlnTyrLeuThrse	176
Db	361	AAATATCGTGTACATATGAAAGTATTA-----	388
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QY 196 l glnaiaalaasnaaleu gl ymet gl uSerLySglnLeuGlnlleHisLeuaspas 216
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 Db 439 C A A G A C C A T A T T A T T G G A T A G T C A A C A A C A T T G A A A G G T T C C T G T G A A A T G A G 498
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 Db 499 A T A C A A G G C T A C A A C A A C C A A C T T G A A G T T A A G A A T T T G A C C A T T T T A C A T A 558
 QY 276 r v a l g i n g l n s e r g l u p h e t y r l e u g l u p r o a n l l e l y t r y v a l p h e g l n v a l a r g c y 296
 Db 559 T G T G C A A C A G T C A G A A T T T C A C T T G G C C A A C A T T A C G T A T T C A G T G A G A T G 618
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 Db 679 T G A A A C A G T T C C C A G G T C A C A T C A A A A G C A T T C C A A C A G A C A T G A C A T G A T T C T G G C T 728
 QY 336 u t h r v a l a s e r l l e s e r t h r g l y h i s l e u t h r s e r a s n a r g l y a s p l l e g l y l e 356
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 QY 356 u l e u l e u g l y m e t l e v a l p h e a l a v a l m e t l e u s e r l l e u s e r l e u l e g l y l e p h 376
 Db 799 T T T A T T G G A A T A T C C T C T T G C T G T A T C T T G C A A T T C T T T G A T T G G A T A T T 858
 QY 376 e a s n a r g s e r p h e a r g t h r g l y l l e y s a r g a r g l l e l e u l e u l e u l e p r o l y s t r p l e 396
 Db 859 T A A C A G A T C A T T C C G A A C T G G A T T A A A A G A A G A G A C T T A T T G T T A T A C C A A A G T G G C T 918
 QY 396 u t r y g l u a s p l l e p r o a s m e t l y s a s e r a s n a r v a l l y m e t l e u g l n l u a n s e 416
 Db 919 T T A T G A A G A T T C C T A T A T G A A A A C A G C A A T G T T G T A A A A T G T T A C A G A A A A T A G 978
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 Db 1039 G A T A A A G A A A T C T T C A T C C A G A C A C A G C C T A C A G A C T A C A G A A G A G A T A T C A G 1098
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 QY 516 u a s p s e r g l y a s n a s n p r o a r g l e u g l n l y s h i s p r o a s n p h e a l a p h e s e r v a l s e r s e 536
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 DEFINITION cds, alternatively spliced.
 ACCESSION AY937252
 VERSION AY937252.1 GI:62870702
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 1618)
 Zhang, X.-Y., Zhang, H.-J., Zhang, Y., Fu, Y.-J., He, J., Zhu, L.-P.,
 Wang, S.-H. and Liu, L.
 Identification and expression analysis of alternatively spliced
 isoforms of human interleukin-23 receptor gene in normal lymphoid
 cells and selected tumor cells
 Immunogenetics 57 (12), 934-943 (2006)
 JOURNAL PUBMED 16372191
 REFERENCE 2 (bases 1 to 1618)
 Zhang, X.-Y., Zhang, Y., Wang, S.-H. and Liu, L.
 AUTHORS Submitted (16-FEB-2005) Microbiology and Etiology, Peking Union
 TITLE Direct Submission
 JOURNAL Medical College, #5 Dong Dan San Tiao, Beijing 100005, China
 FEATURES
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 QY 596 rCysLeuGlyIleValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnI 616
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 Db 1579 TTTGAAAGCCACTTCAATAGATTTCACTTGGAAAAG 1618

Search completed: October 14, 2006, 17:27:19
 Job time : 9899 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 12:54:04 ; Search time 518 Seconds
(without alignments)
10327.220 Million cell updates/sec

Title: US-10-667-289-1
Perfect score: 2857.4
Sequence: 1 gtgtacagggaattccatctg.....gtctggaataaaaaaa 2859

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database:

Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2857.4	100.0	2859	US-09-853-180B-1	Sequence 1, Appl1
2	253.4	8.9	98844	US-09-791-211-10	Sequence 10, Appl1
3	253.4	8.9	143776	US-09-949-001-29	Sequence 29, Appl1
4	253.4	8.9	144034	US-09-949-001-35	Sequence 35, Appl1
5	253	8.9	601	US-09-949-001-581	Sequence 581, Appl1
6	252.8	8.8	601	US-09-949-016-162811	Sequence 162811, Appl1
7	252.4	8.8	90618	US-09-949-016-15964	Sequence 15964, A
8	252	8.8	601	US-09-949-016-70153	Sequence 70153, A
9	251.6	8.8	49301	US-09-949-016-16296	Sequence 16296, A
10	250.8	8.8	168971	US-09-949-016-13807	Sequence 13807, A
11	248	8.7	33478	US-09-949-016-13615	Sequence 13615, A
12	247.8	8.7	8259	US-09-973-378-900	Sequence 900, App
13	247	8.6	75394	US-09-949-016-11754	Sequence 11754, A
14	247	8.6	81001	US-09-750-580-1	Sequence 1, Appl1
15	246.6	8.6	601	US-09-949-016-186635	Sequence 186635, A
16	246.6	8.6	44338	US-09-949-016-12978	Sequence 12978, A
17	246.2	8.6	57859	US-09-949-016-12314	Sequence 12314, A
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20	246	8.6	11863	US-09-949-016-14948	Sequence 14948, A
21	245.4	8.6	60424	US-09-949-016-12115	Sequence 12115, A
22	245.4	8.6	118067	US-09-497-855A-32	Sequence 32, Appl1
23	245.4	8.6	140725	US-09-949-016-17074	Sequence 17074, A

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32	244.4	8.6	37966	US-09-949-016-12566	Sequence 12566, A
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35	244.2	8.5	601	US-09-949-016-17002	Sequence 17002, A
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37	244.2	8.5	37565	US-09-949-002-667	Sequence 667, App
38	244	8.5	51905	US-09-949-002-781	Sequence 781, App
39	244	8.5	51905	US-09-949-016-11921	Sequence 11921, A
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41	244	8.5	325791	US-09-768-185A-1	Sequence 1, Appl1
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ALIGNMENTS

RESULT 1
US-09-853-180B-1
Sequence 1, Application US/09853180B
Patent No. 6756481
GENERAL INFORMATION:
APPLICANT: Charice, Madeline
APPLICANT: Parham, Christi L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: DX01074
CURRENT APPLICATION NUMBER: US/09/853,180B
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 2859
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (119)..(2005)
FEATURE:
NAME/KEY: misc feature
LOCATION: (127)..(127)
OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application as originally filed.
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (188)..(2005)
FEATURE:
NAME/KEY: misc feature
LOCATION: (563)..(563)
OTHER INFORMATION: t means g or a. See page 12, line 36, of patent application as originally filed.
US-09-853-180B-1

Query Match 100.0%; Score 2857.4; DB 3; Length 2859;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTGTACGGGAATTCATTGTGTGGCCACCAAGGCTGCAGCTGCTGAAGT 60

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QY 1861 TGAATATCTTCCAGAACAGACCTGCTCTGATGAAATTTGCTCTGTTTGGGATCGT 1920
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Qy 2641 CGAGTCCAGCTGCTGCAATTTGCTGAAACCTGCTCTTACTTAAATTAAGAAATTTAGCC 2700
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Qy 2701 GGCATGCTGAGGCTGCTGTAATCCAGCTACTTGGAGGCTGAGGCGAGAAATCAC 2760
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Qy 2761 TTGAACGAGAGGAGGAGGTTGCACTGAGCTGAGATTTGTGCACTGCACTCCAGCCTGG 2820
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RESULT 2

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US-09-791-211-10
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 64383
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65468
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65469
; OTHER INFORMATION: unknown

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; NAME/KEY: unsure
; LOCATION: 65470
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65471
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 87130
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 89049
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
US-09-791-211-10

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Query Match 8.9%; Score 253.4; DB 3; Length 98844;
 Best Local Similarity 87.9%; Pred. No. 4.6e-57;
 Matches 275; Conservative 1; Mismatches 37; Indels 0; Gaps 0;

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Qy 2607 GCTGAGTGTGATGATCAGCTGAGGTGAGAGTTGAGTCAAGCTTGGCAATATGCTGA 2666
Db 82068 GCGAGGTGGGTGATCACTGAGTCAAGAGTTGAGACCAAGCTTGTCAATGTGA 82127
Qy 2667 AACCTGTCTCTACTAAATTAAGAAATTAAGCCGAGCATGTGAGGAGGCTTGTATC 2726
Db 82128 AACCTGTCTCTACTAAATTAAGAAATTAAGCCGAGCATGTGAGGAGGCTTGTATC 82187
Qy 2727 CCAGTACTTGGAGGCTGAGGAGGAGATCACTTGAACAGAAAGGAGGTTGAC 2786
Db 82188 CCAGTACTTGGAGGCTGAGGAGGAGATTTCTTGAATCAGGAGGTGAGGTTGAC 82247
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Db 82308 AAAAAAAAAA 82320

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RESULT 3

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US-09-949-001-29
; Sequence 29, Application US/09949001
; Patent No. 6825336
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 143776
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(143776)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-001-29

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Query Match 8.9%; Score 253.4; DB 3; Length 143776;
 Best Local Similarity 87.9%; Pred. No. 5.5e-57;
 Matches 275; Conservative 1; Mismatches 37; Indels 0; Gaps 0;

QY 2547 AAAATAGAAATCATTTAGGCGGAGGCTGGTGGCTCATGCTTGTAAATCCAGACATTTGGTAG 2606
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QY 2607 GCTGAGTGGTGGATCACTGAGGCTGAGAGTTGAGTCCAGCTGAGCTGGCAATATGCTGA 2666
DB 69739 GCGGAGGTGGATGATCACTGAGGCTGAGAGTTGAGAGTCCAGACCTGGTGTAACTGATGA 69798
QY 2667 AACCTGTCTCTACTAAATTTAGCAAAATTTAGCCGCGCATGATGGAGGCTGTGTATC 2726
DB 69799 AACCTGTCTCTACTAAATTTAGCAAAATTTAGCTGGGCGTGGTGGAGGCTGTATC 69858
QY 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACAGAGAGGAGGTTGCAC 2786
DB 69859 CCAGCTACTTGGAGGCTGAGGCGAGAGATTCCTTGAACCTCGGAGGTGAGAGTTGCAG 69918
QY 2787 TGAAGTGAATTTGGCCACTGCACTCCAGCTGGGCAAGAGCAAACTGTCTGGA 2846
DB 69919 TGAAGTGAATTTGGCCACTGCACTCCAGCTGGGCAAGAGCGAACTGTCTGCA 69978
QY 2847 AAAAAAAAAAAAAA 2859
DB 69979 AAAAAAAAAAAAAA 69991

RESULT 4
US-09-949-001-35
Sequence 35, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 144034
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) - (144034)
OTHER INFORMATION: n = A,T,C or G
US-09-949-001-35

Query Match 8.9%; Score 253.4; DB 3; Length 144034;
Best Local Similarity 87.9%; Pred. No. 5.5e-57;
Matches 275; Conservative 1; Mismatches 37; Indels 0; Gaps 0;
QY 2547 AAAATAGAAATCATTTAGGCGGAGGCTGGTGGCTCATGCTTGTAAATCCAGACATTTGGTAG 2606
DB 69679 AAAATAGCAAAATTTTGGCCGGGCGATGGTGGCTCACGCTGTAGTCCAGACATTTGGTAG 69738
QY 2607 GCTGAGTGGTGGATCACTGAGGCTGAGAGTTGAGTCCAGCTGAGCTGGCAATATGCTGA 2666
DB 69739 GCGGAGGTGGATGATCACTGAGGCTGAGAGTTGAGAGTCCAGACCTGGTGTAACTGATGA 69798
QY 2667 AACCTGTCTCTACTAAATTTAGCAAAATTTAGCCGCGCATGATGGAGGCTGTGTATC 2726
DB 69799 AACCTGTCTCTACTAAATTTAGCAAAATTTAGCTGGGCGTGGTGGAGGCTGTATC 69858
QY 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACAGAGAGGAGTTGCAC 2786
DB 69859 CCAGCTACTTGGAGGCTGAGGCGAGAGATTCCTTGAACCTCGGAGGTGAGAGTTGCAG 69918
QY 2787 TGAAGTGAATTTGGCCACTGCACTCCAGCTGGGCAAGAGCAAACTGTCTGGA 2846
DB 69919 TGAAGTGAATTTGGCCACTGCACTCCAGCTGGGCAAGAGCGAACTGTCTGCA 69978

QY 2847 AAAAAAAAAAAAAA 2859
DB 69979 AAAAAAAAAAAAAA 69991

RESULT 5
US-09-949-001-581
Sequence 581, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 581
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-001-581

Query Match 8.9%; Score 253; DB 3; Length 601;
Best Local Similarity 87.5%; Pred. No. 5.6e-58;
Matches 274; Conservative 2; Mismatches 37; Indels 0; Gaps 0;

QY 2547 AAAATAGAAATCATTTAGGCGGAGGCTGGTGGCTCATGCTTGTAAATCCAGACATTTGGTAG 2606
DB 122 AAAATAGCAAAATTTTGGCCGGGCGATGGTGGCTCACGCTGTAGTCCAGACATTTGGTAG 181
QY 2607 GCTGAGTGGTGGATCACTGAGGCTGAGAGTTGAGTCCAGCTGAGCTGGCAATATGCTGA 2666
DB 182 GCGGAGGTGGATGATCACTGAGGCTGAGAGTTGAGAGTCCAGACCTGGTGTAACTGATGA 241
QY 2667 AACCTGTCTCTACTAAATTTAGCAAAATTTAGCCGCGCATGATGGAGGCTGTGTATC 2726
DB 242 AACCTGTCTCTACTAAATTTAGCAAAATTTAGCTGGGCGTGGTGGAGGCTGTATC 301
QY 2727 CCAGCTACTTGGAGGCTGAGGCGAGAGATCACTTGAACAGAGAGGAGTTGCAC 2786
DB 302 CCAGCTACTTGGAGGCTGAGGCGAGAGATTCCTTGAACCTCGGAGGTGAGAGTTGCAG 361
QY 2787 TGAAGTGAATTTGGCCACTGCACTCCAGCTGGGCAAGAGCAAACTGTCTGGA 2846
DB 362 TGAAGTGAATTTGGCCACTGCACTCCAGCTGGGCAAGAGCGAACTGTCTGCA 421
QY 2847 AAAAAAAAAAAAAA 2859
DB 422 AAAAAAAAAAAAAA 434

RESULT 6
US-09-949-016-162811/c
Sequence 162811, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 162811
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-162811

Query Match
Best Local Similarity 83.5%; Score 252.8; DB 3; Length 601;
Matches 284; Conservative 2; Mismatches 54; Indels 0; Gaps 0;

QY 2520 TAAATTAATGCTGTAATTTCTTAAATAGATCATAGCCAGCGCTGTGCTC 2579
DB 400 TCAAGAAATTAATCCATTGGGGCTTGAAGAGAAAGGATCGGGTGTGCTC 341
QY 2580 ATGCTTGAATCCAGCATTTGGTAGGCTGAGGTGGTGAATCACTGAGTCAGAGT 2639
DB 340 ATGCTTGAATCCAGCATTTGGTAGGCTGAGGTGGTGAATCACTGAGTCAGAGT 281
QY 2640 TCGAGTCAGCTGGCCCAATATGCTGAACCTGCTCTAATAATTAACAAATTAGC 2699
DB 280 TCGAAACAGCTGGCCCAATGCTGAACCTGCTCTAATAATAATTAACAAATTAGC 221
QY 2700 CGGCGATGCTGGCAGCTGCTTGAATCCAGCTACTTGGAGGCTGAGGAGAGATCA 2759
DB 220 TGGGCAAGGTGGCAGGCGCTGTATCCAGCTACTTGGAGGCTGAGGAGAGATCA 161
QY 2760 CTTGAACCAAGAGGAGGAGGTTGCACTGAGCTGAGATTTGTCACCTCCAGCTG 2819
DB 160 CTTGAACCCGAGGAGGAGGTTGCACTGAGCTGAGATTTGTCACCTCCAGCTG 101
QY 2820 GGCAACAGAGCAAACTCTGCTGGAATAAAAAAAAAA 2859
DB 100 GGGAACAAGAGCAAACTCTGCTCAAAAAAAAAA 61

RESULT 7

US-09-949-016-15964/C
Sequence 15964, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15964
LENGTH: 90618
TYPE: DNA
ORGANISM: Human
US-09-949-016-15964

Query Match
Best Local Similarity 85.4%; Score 252.4; DB 3; Length 90618;
Matches 280; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

QY 2532 TGAATATTTCTTAAATAGATCATTAAGCCAGGCGTGGCTCATGCTGTATATC 2591
DB 72673 TTATTAATTTGCATTAATAATGTAAGTAACGCGCGGCGGTGCTCATGCTGTATATC 72614
QY 2592 CCAAGCACTTTGGTAGGCTGAGGTGGTGAATCACTGAAGTCAGAGATTGAGTCCAGCC 2651
DB 72613 CCAAGCACTTTGGTAGGCTGAGGTGGTGAATCACTGAAGTCAGAGATTGAGTCCAGCC 72554

QY 2652 TGGCAATATGCTGAACCTGCTCTACTAATAATTAACAAATTAGCCGCGCATGTGG 2711
DB 72553 TGGCAATATGCTGAACCTGCTCTACTAATAATTAACAAATTAGCCGCGCATGTGG 72494
QY 2712 CAGGTGCTTGAATCCAGCTACTTGGAGGCTGAGGAGAGATCACTTGAACAGGA 2771
DB 72493 CAGGCGCTGTAATCCAGCTACTTGGAGGCTGAGGAGAGATCACTTGAACAGGA 72434
QY 2772 AGGCAAGGTTGCACTGAGTGAATTTGCTCACTGATCTCCAGCTGGGCAACAGC 2831
DB 72433 AGGCAAGGTTGCACTGAGTGAATTTGCTCACTGATCTCCAGCTGGGCAACAGC 72374
QY 2832 AAACTGCTGTAATAAAAAAAAAA 2859
DB 72373 GAGACTCATCTCAAAAAAAAAA 72346

RESULT 8

US-09-949-016-70153
Sequence 70153, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70153
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-70153

Query Match
Best Local Similarity 83.9%; Score 252; DB 3; Length 601;
Matches 282; Conservative 2; Mismatches 52; Indels 0; Gaps 0;

QY 2518 AGTAATAATAATGCTGAATAATTTCTTAAATAGATCATTAAGCCAGGCGTGTGGC 2577
DB 82 AGTAATAATAATGCTGAATAATTTCTTAAATAGATCATTAAGCCAGGCGTGTGGC 141
QY 2578 TCATGCTTGAATCCAGCATTTGGTAGGCTGAGGTGGTGAATCACTGAGTCAAGA 2637
DB 142 TCATGCTTGAATCCAGCATTTGGTAGGCTGAGGTGGTGAATCACTGAGTCAAGA 201
QY 2638 GTTCGAGTCAGCTGGCCCAATATGCTGAACCTGCTCTAATAATTAACAAATTGA 2697
DB 202 GTTCGAGTCAGCTGGCCCAATATGCTGAACCTGCTCTAATAATTAACAAATTGA 261
QY 2698 GCCGCGATGCTGGCAGGTGCTTGAATCCAGCTACTTGGAGGCTGAGGAGAGAT 2757
DB 262 GCTGGGCGTGTGGCAGGCGCTGTATTAACAGCTACTGAGGAGGCTGAGGAGAGAT 321
QY 2758 CATTTGAACCAAGAGGAGGTTGCACTGAGCTGAGATTTGGCCACTGCTCCAGCC 2817
DB 322 CGCTTGAACCTGGAGAGGAGGTTGCACTGAGCTGAGATTCGTCATGCTGCTCCAGCC 381
QY 2818 TGGCAACAAGAGCAAACTGCTGGAATAAAAAA 2853
DB 382 TGGCAACAAGAGCAAACTGCTGGAATAAAAAA 417

RESULT 9


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Sequence 11754, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11754
LENGTH: 75394
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(75394)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11754
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Query Match 8.6% Score 247; DB 3; Length 75394;
Best Local Similarity 86.6%; Pred. No. 2,1e-55;
Matches 271; Conservative 1; Mismatches 41; Indels 0; Gaps 0;
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QY 2547 AATAAGATCATTCATGAGCCAGGCGTGGTGTGCTCATGCTTGAATCCAGACCTTGTAG 2606
DB 68328 AATAAGATTAAGAAATAGGCGGCGTGGTGTGCTCATGAGCTTGAATCCAGACCTTGTAG 68387
QY 2607 GCTGAGTGTGTGATCATCTGAGGTGAGAGTTCCAGCTTCCAGCTTCCAAATATGCTGA 2666
DB 68388 GCTGAGTGTGTGATCATCTGAGGTGAGAGTTCCAGCTTCCAGCTTCCAAATATGCTGA 68447
QY 2667 AACCTGTCTTACTAATAAATATAGCCGGCCATGCTGGAGGTGCTTATC 2726
DB 68448 AACCTGTCTTACTAATAAATATAGCCGGCCATGCTGGAGGTGCTTATC 68507
QY 2727 CCAAGCTACTTGGAGGCTGAGGCGAGAAATCACTTGAACCAAGAGGAGAGGTGAC 2786
DB 68508 CCAAGCTACTTGGAGGCTGAGGCGAGAAATCACTTGAACCAAGAGGAGAGGTGAC 68567
QY 2787 TGAGCTGAGATTGTCCTGCACTGCACTTGGGCAACAAGACAAATCTTGTCTGA 2846
DB 68568 TGAGCTGAGATTGTCCTGCACTGCACTTGGGCAACAAGACAAATCTTGTCTGA 68627
QY 2847 AAAAAAAAAA 2859
DB 68628 AAAAAAAAAA 68640
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RESULT 14

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US-09-750-580-1/c
Sequence 1, Application US/09750580
Patent No. 6455280
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas, Mline Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Kibets-Red, Dana
APPLICANT: Salter-Cld, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.US2.CIP
CURRENT APPLICATION NUMBER: US/09/750,580
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CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patenc.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc.feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
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LOCATION: 929..949
OTHER INFORMATION: 20-828-pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 17-42-tp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42-pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42-tp complement
NAME/KEY: primer_bind
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NAME/KEY: primer_bind
LOCATION: 15460..15482
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OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
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OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644..76664
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NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
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NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe

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US-09-750-580-1
Query Match      8.6%; Score 247; DB 3; Length 81001;
Best Local Similarity 86.6%; Pred. No. 2.2e-55;
Matches 271; Conservative 1; Mismatches 41; Indels 0; Gaps 0;

QY 2547 AAAATAGAAATCAATAGCCAGGCGGTGGGCTCATGCTTGTATATCCACAGCAGCTTTGGTAG 2606
DB 65051 ATAAAGAAATGTGTGGCCAGGTGCAAGTGGCTCAGCGCTGTATATCCACAGCAGCTTTGGGAG 64992
QY 2607 GCTGAGGTGAGTGGATCACTGAGGTCAAGATTGAGTTCACGCTGGCCAAATATGCTGA 2666
DB 64991 GCCAAGGTGGGTGATCACTGAGGTCAAGATTGAGATCAACGAGCCTGGCCAAATATGCTGA 64932
QY 2667 AACCTGTCTCTACTAAAAATTACAAAAATTAGCCGCGCATAGTGGCAAGTCTTGTATATC 2726
DB 64931 AACCCCGCTCTATTTAAAAATAACAAAAATTAGCCGCGCATAGTGGCAGAGCCTGTATATC 64872
QY 2727 CCAGTATATTGGGAGGCTGAGGCGAGGAATATCATTTGAATCCAGGAAGGACAGAGTTGCAC 2786
DB 64871 CCAGTACTTCAGAGGCTGAGGCGAGGAATATCATTTGAATCCGCGAGGCGAGGTTGCAG 64812
QY 2787 TGAGCTGAGATTGTGSCCACTGACATCCAGCCTGGGCAACAAGAGAAAACTGTCTGGA 2846
DB 64811 TGAGCTGAGATTGGCCCACTGACATCCAGCCTGAGGAGCAAGAGGAGACTGTATCA 64752
QY 2847 AAAAAAAAAAAAAA 2859
DB 64751 AAAAAAAAAAAAAA 64739

RESULT 15
US-09-949-016-186635/c
US-09-949-016-186635, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 186635
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-186635

Query Match      8.6%; Score 246.6; DB 3; Length 601;
Best Local Similarity 81.7%; Pred. No. 2.9e-56;
Matches 282; Conservative 2; Mismatches 61; Indels 0; Gaps 0;

QY 2513 CTGTAGTAAATAATAGCTGAAAAATTTCTTTAAAAATGAAATCATTAGGCCAGGCGTG 2572
DB 369 CTGGAGTACACACTTACCAAAACATTAATGATACCTAAGAAATGTTGGCCGCGCTG 310
QY 2573 GTGGCTCATGCTTGAATTCACGACCTTTGGTAGGCTGAGGRTGATCACTGAGGT 2632
DB 309 GTGGCTCATGCTTGAATTCACGACCTTTGGTAGGCTGAGGRTGATCACTGAGGT 250
QY 2633 CAGAGATTGAGTCCAGGCTGAGCCATATGCTGAAACCCCTGTCTACTTAAATTTACAA 2692
DB 249 CAAAGATTGAGACCAAGCTGATACCAACATAGTAAATCTGTCTTAAATTTACAA 190
QY 2693 AATTAGCCGCGCATAGTGGCAGAGTCTTGTATATCCAGCTACTTGGAGGCTGAGGACG 2752

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Run on: October 14, 2006, 14:40:43 ; Search time 1964 Seconds

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Perfect score: 3326

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Fgapop 6.0 , Fgapext 7.0	
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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 3784340

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-DB=Published.Applications.NA.Main -OPMT=fastap -SUFFIX=p2n.rnpbm
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-MATRIX=blonum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
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-HEADING=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs803h
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA.Main.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3324	99.9	2859	9	US-10-797-157-5	Sequence 5, Appl1
3	3324	99.9	2859	9	US-10-720-026-1	Sequence 1, Appl1
4	3324	99.9	2859	10	US-10-667-289-1	Sequence 1, Appl1
5	3324	99.9	2859	10	US-10-667-290-1	Sequence 1, Appl1
6	3314	99.6	1890	3	US-09-972-708-20	Sequence 20, Appl1
7	3314	99.6	1890	8	US-10-715-667-20	Sequence 9, Appl1
8	3314	99.6	1890	3	US-10-105-930-9	Sequence 19, Appl1
9	3314	99.6	2830	6	US-09-972-708-19	Sequence 19, Appl1
10	3314	99.6	2830	8	US-10-715-667-19	Sequence 19, Appl1
11	3292	99.0	2123	6	US-10-105-930-5	Sequence 5, Appl1
12	2952	88.8	1698	3	US-09-972-708-22	Sequence 22, Appl1
13	2952	88.8	1698	8	US-10-715-667-22	Sequence 22, Appl1
14	2280.5	68.6	1935	8	US-09-972-708-29	Sequence 29, Appl1
15	2280.5	68.6	1935	8	US-10-715-667-29	Sequence 29, Appl1
16	2192	65.9	1301	6	US-10-105-930-7	Sequence 7, Appl1
17	2175	65.4	1479	6	US-10-105-930-3	Sequence 3, Appl1
18	2039	61.3	1155	6	US-10-247-463-1	Sequence 1, Appl1
19	2039	61.3	1155	13	US-11-016-106-1	Sequence 1, Appl1
20	1868	56.2	1071	3	US-09-972-708-24	Sequence 24, Appl1
21	1868	56.2	1071	8	US-10-715-667-24	Sequence 24, Appl1
22	1747	52.5	1152	6	US-10-247-463-3	Sequence 3, Appl1
23	1747	52.5	1152	13	US-11-016-106-3	Sequence 3, Appl1
24	1695	51.0	1784	6	US-10-105-930-1	Sequence 1, Appl1
25	335	10.1	637	6	US-10-027-632-210413	Sequence 210413,
26	335	10.1	637	7	US-10-027-632-210413	Sequence 210413,
27	286	8.6	360	6	US-10-105-930-23	Sequence 23, Appl1
28	268	8.1	1293	10	US-10-750-185-59162	Sequence 59162, A
29	268	8.1	1293	10	US-10-750-623-59162	Sequence 59162, A
30	256.5	7.7	2995	7	US-10-425-529-17	Sequence 17, Appl1
31	256.5	7.7	2995	9	US-10-645-012-17	Sequence 17, Appl1
32	250	7.5	412	3	US-09-864-761-16612	Sequence 16612, A
33	225.5	6.8	3274	16	US-11-136-527-2009	Sequence 2009, Ap
34	221	6.6	4023	9	US-10-398-666-11	Sequence 11, Appl1
35	216	6.5	4040	10	US-10-370-7158-67	Sequence 67, Appl1
36	216	6.5	4040	10	US-10-929-182-19	Sequence 19, Appl1
37	210	6.3	2838	3	US-10-450-763-12224	Sequence 12224, A
38	209	6.3	3085	10	US-09-829-472A-8	Sequence 8, Appl1
39	209	6.3	3085	7	US-10-177-293-229	Sequence 229, App
40	209	6.3	3085	7	US-10-172-118-736	Sequence 736, App
41	209	6.3	3085	7	US-10-295-027-73	Sequence 73, Appl1
42	209	6.3	3085	8	US-10-058-870A-31	Sequence 31, Appl1
43	209	6.3	3085	8	US-10-342-887-736	Sequence 736, Appl1
44	209	6.3	3085	8	US-10-641-643-1131	Sequence 1131, Ap
45	209	6.3	3358	6	US-10-116-802-208	Sequence 208, App

ALIGNMENTS

RESULT 1
US-09-853-180-1
Sequence 1, Application US/09853180
Publication No. US20030017617A1
GENERAL INFORMATION:
APPLICANT: Chirica, Madeline
APPLICANT: Parham, Christi L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: DX01074
CURRENT APPLICATION NUMBER: US/09/853,180
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2859
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (119)..(2005)
OTHER INFORMATION:

US-09-853-180-1

Alignment Scores:

Pred. No.:	0	length:	285
Score:	324.00	Matches:	629
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	3	Gaps:	0

US-10-667-289-2 (1-629) x US-09-853-180-1 (1-2859)

[illegible]

Db	1019	AAAAGTAACTGGAGCGCTTGAGATTCACCGTTTTCATATAAAACCACTGAAACAGTTCC	1078
Oy	321	GlnValThiSerIyValApeGlnHLeaPThrTrpAsnSerGlyLeuThrValAlaSer	340
Db	1079	CAGGTCAATCAAAAGCAATTCACAACAGAACATGAAATTCGGGCTTACAGATGGCTTCC	1138
Oy	341	IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet	360
Db	1139	ATCTCTACAGGGCACTTACTTCTGCACACACAGAGACACTTGGACTTTTATTGGGATG	1198
Oy	361	IleValPheAlaValMetLeuSerIleLeuSerIleGlyIlePheAsnArgSerPhe	380
Db	1199	ATCGTCTTCTGCTTATGTTGTGTCAAATCTTTCCTTGGATTGGATATTAAACAGATCATTC	1258
Oy	381	ArgThrGlyIleIysArgArgIleLeuLeuLeuIleProIysTrpLeuTyroGlyAspIle	400
Db	1259	CGAATCGAGATTAATAAAGAGATCTTATGTGTATACCAAGAGGCTTATTGAAGATATT	1318
Oy	401	ProAsnMetIyAsnSerAsnValValIleMetLeuGlnIubAsnSerGlyLeuMetAsn	420
Db	1319	CCTAATATGAAAAACAGCAATGTTGTGAAATGCTTACAGGAAATATGAACTTATGAAT	1378
Oy	421	AsnAsnSerSerGlyGlnValLeuTyroValAspProMetIleThrGlyIleYsGlnIle	440
Db	1379	AATATATTCAGATGAGCGAGGTCTCTATATGTTGATCCCATGATACAGAGATTAAGAAATC	1438
Oy	441	PheIleProGlnHisIyAspProThrAspTyroIleYsGlyIubAsnThrGlyProLeuGlyThr	460
Db	1439	TTTATCCCAAGAACCAAGCTTACAGACTACAGAAGAGAAATACAGAACCCCTGGAGACA	1498
Oy	461	ArgAspTyroProGlnAsnSerLeuPheAspAsnThrThrValValTyroIleProAspLeu	480
Db	1499	AGAACACTACCCGCAAACTCGCTATATGACAATCTCAAGTTGATATATATTCCTGAACTC	1558
Oy	481	AsnThrGlyTyroIyAspProGlnIleSerAsnPheLeuProGlyIySerHisLeuSerAsn	500
Db	1559	AACCTGGATATTAACCCCAATTTCCAAATTTTCTGCTGAGGAGAACCATCTCAGCAAT	1618
Oy	501	AsnAsnGlnIleThrSerLeuThrLeuIyAspProProValAspSerLeuAspSerGlyAsn	520
Db	1619	AATATATGAATTAATCTTCTTAAACCTTAAACACCAAGTTGATTCCTTAGACTCAGAGAAAT	1678
Oy	521	AsnProArgLeuGlnIyHisIAspProAsnPheAlaPheSerValSerSerValAsnSerLeu	540
Db	1679	AATCCCAAGGTACAAAGACATCTTAATTTGGCTTTTCTGTTTCAAGTGAATTCATCTA	1738
Oy	541	SerAsnThrIlePheLeuGlyGlyLeuSerLeuIleLeuAsnGlnIyGlyIyCysSerSer	560
Db	1739	AGCAACACAAATTTCTTGGAGATTAAGCTCATATTAAATCAAGAGAAATGACATTCCT	1798
Oy	561	ProAspIleGlnAsnSerValGlyGlyGlyIubThrThreLeuLeuGlnAsnAspSerPro	580
Db	1799	CCTGACATACAAAACCTACGTAGAGAGAGAAACCCACATGCTTTGGAAAAATGATTCACCC	1858
Oy	581	SerGlyThrIleProGlyGlnIubThrLeuLeuProAspGlyPheValIserCysLeuGlyIle	600
Db	1859	AGTAAACTATTCCAGAACAGACCCCTGCTTCTATGAATTTGCTCTCTGTGGGATC	1918
Oy	601	ValAsnGlyIubLeuProSerIleAsnThrTyroPheProGlnAsnIleLeuGlySerHis	620
Db	1919	GTGAATAGAGAGTGGCCATCTTAATTAATCTATTTCACAAATATTTTGGAAAGCCAC	1978
Oy	621	PheAsnArgIleSerLeuLeuGlnIyS 629	
Db	1979	TTCAATAGGAATTCACCTTGGAAAAG 2005	

RESULT 2
US-10-797-157-5
; Sequence 5, Application US/10797157
; Publication No. US2004022369A1
; GENERAL INFORMATION:
; APPLICANT: Ofc, Martin

APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS
FILE REFERENCE: D06022US01
CURRENT APPLICATION NUMBER: US/10/797,157
CURRENT FILING DATE: 2004-03-09
PRIOR APPLICATION NUMBER: U.S. 60/453,672
PRIOR FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 2859
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (119)..(2005)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (188)..(2005)
US-10-797-157-5

Alignment Scores:

Pred. No.:	0	Length:	2859
Score:	3324.00	Matches:	629
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	9	Gaps:	0

US-10-667-289-2 (1-629) x US-10-797-157-5 (1-2859)

Qy 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
Db 119 ATGATACAGTCACATTAATCAAGGATGCAATGAGCCTTAACATCTTCAAGCTGG 178
Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
Db 179 TGTATGAGGAATTAACAATATAAATGCTGCTGCGCAACCTGGTGAACCGCCACA 238
Qy 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleValAsnCysGln 60
Db 239 ATTTTAAAGTGGGTATGAATATCTCTATATATGCGAAGCAGCAATTAAGAACTGGCAA 298
Qy 61 ProArgLeuHisPheTyrLeuAsnGlyTyrIleGluArgPheGlnIleThrArgIle 80
Db 299 CCAAGGAACCTCAATTTTATAAATGCAATCAAGAAAGATTCAATCAAGAAAT 358
Qy 81 AsnLeuThrThrAlaArgLeuTyrTyrLeuAsnPheLeuGluProHisAlaSerMetTyr 100
Db 359 AATTAACAACAGCTCGCTTGGTATTAATAAATCTTCTGAAACCAATGCTTCTATGTAC 418
Qy 101 CysThrAlaGluCysProLeuHisPheGlnGluThrLeuIleCysGlyValAspIleSer 120
Db 419 TGCCTCTGTAATGCCAAACATTTTCAAGAGACACTGATATGGAATAAGACATTTCT 478
Qy 121 SerGlyTyrProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
Db 479 TCTGGAATATCCGCAAGATATCTGATGAAGTAACCTGTGCATTTAAGAAATATTCAGGC 538
Qy 141 AsnMetThrCysThrTrpAsnAla**LysLeuThrTyrIleAspThrIleValVal 160
Db 539 AACATGACTTGCACCTGGAATGCTRGAAAGCTCACTACATAGACAAATAATGCTGTA 598
Qy 161 HisValLysSerLeuGluThrGluGluGluGluGluGluGluGluGluGluGluGlu 180
Db 599 CATCTGAAGGTTTAAAGACAGAAAGAGCAACAGATATCTCAAGCTAATATTAAC 658
Qy 181 IleSerThrAspSerLeuGluGluGlyLysLeuTyrIleValTyrValGlnAlaAsn 200
Db 659 ATCTCCACTGATTAATCAAGGTGGCAAGAGTACTTGGTTGGGTTCCAGCGCAAC 718
Qy 201 AlaLeuGlyMetGluSerLysGluLeuGlnIleHisLeuAspAspIleValIlePro 220

Db 719 GCATAGCATGGAAGATCAAAACATGCAATTCACCTGATGATATAGTACT 778
Qy 221 SerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db 779 TCTGCAAGCTGATTTTCCAGGCTGAGACTTAATATCTACAGGCCCAAGACCAATAT 838
Qy 241 TyrTrpAspSerGlnThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
Db 839 TATGGGATAGTCAACCAACAAATGAAAGGTTTCTGTAATATGATATCAAGCTACA 898
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
Db 899 ACAAAACCAACTGGAATGTTAAAGAAATTTGACCAATTTTACATATGTCACACATCA 958
Qy 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db 959 GAATTTCTACTTGGAGCCAAACATTAAGTACGATTTCAAGTACATCAAGAAACAGGC 1018
Qy 301 LysArgTyrTrpGluProTrpSerSerProPhePheHisLysThrProGluThrValPro 320
Db 1019 AAAAGTACTGGCAGCCTTGGAGTTCAACGTTTTTTCATAAACACCTGAACAGTTCCC 1078
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db 1079 CAGGTCAATCAAAAGCAATTCACATGACATGGAATTTCTGGCTTAACAGTTGCTTCC 1138
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
Db 1139 ATCTTACAGGCACTTACTTCTGACACAGAGGACATGAGCTTTATTTATGGAAATG 1198
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1199 ATCGTCTTCTGTAATGTTGTCAATCTTCTTGAATGGAAATTAACAGATCAATTC 1258
Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
Db 1259 CGAACTGGATTTAAAGAAAGATCTTATGTATATACAAAGTGGCTTTATGAAGATAT 1318
Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420
Db 1319 CTTAATATGAAACACAGCAATGTTGTAAATGCTACAGAAATATGAACTTATGAT 1378
Qy 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440
Db 1379 AATTAATCCAGTACAGAGCTCTATATGTTGATCCATGATTAACAGATTAAGAAATC 1438
Qy 441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
Db 1439 TTCATCCAGAACCAAGCCTTACAGACTACAAAGAGAGATACAGACCCTGGAACA 1498
Qy 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
Db 1499 AGAGACTACCCGCAAACTGCTATTCGACAAATACACAGTGTATATATCCGAACTC 1558
Qy 481 AsnThrGlyTyrLysProGluIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500
Db 1559 AACACTGGAATTAACCCCAATTTTCAATTTTCTGCTACAGGAAACCTTCACGAAAT 1618
Qy 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db 1619 AATTAATGAATTAATCTTCAACACTTAACCAACAGTGTATTCCTTAAGACTCAGAAAT 1678
Qy 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db 1679 AATCCAGGTTAAACAAAGCAATCTTAATTTGCTTTTCAAGTGAATTCACATA 1738
Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyCysSerSer 560
Db 1739 AGCAACCAATATTTCTTGAAGAAATTAAGCTCATATTAATCAAGAGATCAAGTTCT 1798
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
Db 1799 CTTGACATACAAACATCAAGTACAGAGAAACCAACATGCTTTTGGAAATGATTCACCC 1858

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Qy 581 SerGluThrIleProGluGlnThrIleuLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1859 AGTGAACACTATTCAGAAACAGACCCCTCTCTCATGATGATTCCTCTGTTGGGATC 1918
Qy 601 ValAsnGluLeuLeuProSerIleAsnThrIleThrProGlnAsnIleLeuGluSerHis 620
Db 1919 GTGATATAGAGAGTTGGCATCTATTAATATCTATTTCCACAAATATTTGGAAAGCCAC 1978
Qy 621 PheAsnArgIleSerLeuLeuGluLys 629
Db 1979 TTCAATAGCATTTCACTTTGGAAAG 2005

RESULT 3
US-10-720-026-1
; Sequence 1, Application US/10720026
; Publication No. US20040258686A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madeline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX0107431K
; CURRENT APPLICATION NUMBER: US/10/720,026
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(2005)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (188)..(2005)
US-10-720-026-1

Alignment Scores:
Pred. No.: 0 Length: 2859
Score: 3324.00 Matches: 629
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: Gaps: 0

US-10-667-289-2 (1-629) x US-10-720-026-1 (1-2859)
Qy 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuThrIleuPheSerTrp 20
Db 119 ATGATATCAKGTCACTATTCATGAGATGACAGTAAATAGCCCTTACATCACTCTTACGCTGG 178
Qy 21 CysHisGlyIleIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
Db 179 TGTCAATGAGGAATTAACAATATTAACGTCTGGCCACATCTGGTGAACAACGCCACA 238
Qy 41 IlePheIleMetGlyMetAsnIleSerIleTrpCysGlnAlaAlaIleLysAsnCysGln 60
Db 239 ATTTTAAAGATGGGTATGAATATCTCTATATATGCGCAACAGCAATTAAGAACTGCCAA 298
Qy 61 ProArgLysLeuHisPheTrpLysAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80
Db 299 CCAAGGAACTTCACTTTTAAATAATGCAATCAAGAAAGATTTCAATCAACAGGATTT 358
Qy 81 AsnLysThrThrAlaArgLeuTrpTrpLysAsnPheLeuGluProHisAlaSerMetTrp 100
Db 359 AATTAACAACAAGCTGGCTTGTGTATTAATAACTTTCTGGAACACACATGCTTCTATGTAC 418
Qy 101 CysThrAlaGluCysProLysHisPheGlnGlnThrLeuIleCysGlyLysAspIleSer 120

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Db 419 TGCACGCTGAATAGTCCCAAACTTTTCAGAAACACTGATATGTGAAAAAGCACTTCT 478
Qy 121 SerGlyTrpProProAspIleProAspGluValIleCysValIleIleTrpGluTrpSerGly 140
Db 479 TCTGATATCTCCGCAAGATATCTCTGATGAAGTAACTGCTCTATTTATGATATTTCAAGC 538
Qy 141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTrpIleAspThrLysTrpValVal 160
Db 539 AACATGACTTGACCTGGAATGCTGGAGAGCTCACTCACTAATACAAATAATCGTGTA 598
Qy 161 HisValLysSerLeuGluThrGluGluGluGlnGlnIleThrIleuThrSerSerTrpIleAsn 180
Db 599 CATGTAGAGAGTTAGAGACAGAAAGAACCAAGATATCTCACTCAACCTATATTAAC 658
Qy 181 IleSerThrAspSerLeuGlnGlyLysLysTrpLeuValTrpValGlnAlaAlaAsn 200
Db 659 ATCTCCACTATTCATTACAAAGGTGGCAAGATGATCTGTTGGGTCCAAAGCAGCAAC 718
Qy 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
Db 719 GCACTAGGAGTGAAGAGTCAAAACAACTGCAATTCACCTGGATGATATAGTATGATCCT 778
Qy 221 SerIleAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db 779 TCTGCAAGCCGTCAATTCAGAGGCTGAGACTATTAATGCTACAGTGCACCAAGCCATATT 838
Qy 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTrpLysAlaThr 260
Db 839 TATTTGGATATGTCMAACACAAATTGAAGAGTTTCTGTGAAATGATCAAGGCTACA 898
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrValGlnGlnSer 280
Db 899 ACAACCAACTGGAATGTTAAAGAAATTGACACCAATTTACATATGCAACAGTCA 958
Qy 281 GluPheTrpLeuGluProAsnIleLysTrpValPheGlnValArgCysGlnGluThrGly 300
Db 959 GAATTCATCTTGAGGCCAAACATTAGTACGTATTCAGTGAAGATGTCAGAAACAGGC 1018
Qy 301 LysArgGlyTrpGlnProTrpSerSerProPheHisLysThrProGluThrValPro 320
Db 1019 AAAAGTACTGGACGCTTGAGAGTTCACCGTTTTCATATAAACACTGAAACAGTTCCC 1078
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db 1079 CAGGTCAACATCAAAAGATCTCAACATGACATGAAATCTGGGCTTAACAGTGGCTTCC 1138
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
Db 1139 ATCTCTACAGGGCACTTACTCTGACACACAGAGAGACATTTGACTTTATTTGGGATG 1198
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1199 ATGCTCTTCTGCTGTTATGTTGTCAATTCCTTTCTTGAATGGAATATTAACAATCATTC 1258
Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTrpGluAspIle 400
Db 1259 CGAACTGGAGATTAAGAAGATCTTATGTTATATCAAAAGTGGCTTTATGAAGATATT 1318
Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLysAsnSerGluLeuMetAsn 420
Db 1319 CCTAATATGAAAAACAGCAATGTTGMAAATCTACAGGAAAAATGATGAACCTTAAGAAAT 1378
Qy 421 AsnAsnSerSerGluGlnValIleLysTrpValAspProMetIleThrGluIleLysGluIle 440
Db 1379 AATTAATTCAGTAGAGAGGCTCTATATGTTGATCCCATGATTTACAGAGATTAAGAATAATC 1438
Qy 441 PheIleProGluHisLysProThrAspTrpLysLysGluAsnThrGlyProLeuGluThr 460
Db 1439 TTCACTCCAGAACCAAGCCTTACAGACTTACAAAGAGAGATACAGGACCCCTGGAGACA 1498
Qy 461 ArgAspTrpProGluAsnSerLeuPheAspAsnThrThrValValIleProAspLeu 480

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Db      1019 AAAAGGACTGGCAGCTTGGAGTTCACCTTTTTCATATAACCTGAAACAGTCCC 1078
Qy      321 GlnValThrSerValAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db      1079 CAGGTCCATCAAAAAGCATTCACACATGACATGAAATTCGGGCTTAACAGTTGCTTCC 1138
Qy      341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
Db      1139 ATCTCTACAGGGACCTTACTTCTGACACAGAGGACACATTTGAGACTTTTATTGGGAATG 1198
Qy      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db      1199 ATGCTCTTCTGCTTATGTTGTCATTCCTTTCCTTGTGATGAGATTTAAACAGATCAATC 1258
Qy      381 ArgThrGlyIleLeuValArgGlyIleLeuLeuIleProGlySerTrpLeuArgIle 400
Db      1259 CGAACTGGGATTTAAAGAGATCTTATGTTATACCAAAGTGGCTTTATGAAAGATATT 1318
Qy      401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLubAsnSerGlyLeuMetAsn 420
Db      1319 CTTATATGAAAAACACATGTTGTGAAAATGCTACAGAAAATAGTGAATTAATGAT 1378
Qy      421 AsnAsnSerSerGlyGlnValLeuTyrValAspProMetIleThrGlyIleGlyIle 440
Db      1379 AATATATCCAGTGCAGAGTCTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1438
Qy      441 PheIleProGlyHisLysProThrAspTyrLysLysGlyLubAsnThrGlyProLeuGlnThr 460
Db      1439 TTTATCCCAAGAACCAAGCCTTACAGACTTACAGAGAGAAATACAGAGCCCTGGAGACA 1498
Qy      461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
Db      1499 AGAGACTACCCGCAAACTGGCTATTGACATATCTACAGTTGATATATATTCCTGATCTC 1558
Qy      481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGlyLysSerHisLeuSerAsn 500
Db      1559 AACCTGATATTAACCCCAATTTCAATTTCTGCTGAGGAAACCCATCTCAGCAAT 1618
Qy      501 AsnAsnGlnIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db      1619 AATATGAAATTTACTTCTTAACCTTAACCAACACAGTTGATTCCTAGACTCAGGAAT 1678
Qy      521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db      1679 AATCCCAAGTTACAAAGACATCCAAATTTGCTTTCTGTTCAAGTGAATTCCTA 1738
Qy      541 SerAsnThrIlePheLeuGlyGlyLeuSerLeuIleLeuAsnGlnGlyLysSerSer 560
Db      1739 AGCAACACAAATATTTCTTGGAGATTAAGCTCATATTAATCAAGAGATGCAATCTCT 1798
Qy      561 ProAspIleGlnAsnSerValGlnGlnGlnThrThrMetLeuGlnLubAsnAspSerPro 580
Db      1799 CCGTACATTAACAACTAGTAGAGAGAGAAACCAACAGCTTTGGAAAAATGATTCACC 1858
Qy      581 SerGlnThrIleProGlnGlnThrLeuLeuProAspGlnPheValSerCysLeuGlyIle 600
Db      1859 AGTGAACATATTCAGAAACAGACCCCTGCTTCGATGAATTTGTCTCTGTTGGGAATC 1918
Qy      601 ValAsnGlnGlnLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlnSerHis 620
Db      1919 GTGATATAGAGGTGGCATCATTAATTAATTAATTTCCACAAATATTTGGAAAGCCAC 1978
Qy      621 PheAsnArgIleSerLeuLeuGlnLys 629
Db      1979 TTCAATAGAGATTCACTCTTGGAAAG 2005

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RESULT 5
US-10-667-290-1
; Sequence 1, Application US/10667290
; Publication No. US20050100918A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madeline

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; APPLICANT: Parham, Christl L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074
; CURRENT APPLICATION NUMBER: US/10/667,290
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/853,180B
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(2005)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (127)..(127)
; OTHER INFORMATION: k means g or t/u. See page 12, line 34, of patent application as
; OTHER INFORMATION: originally filed.
US-10-667-290-1

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Alignment Scores:
Pred. No.: 0 Length: 2859
Score: 3324.00 Matches: 629
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: Gaps: 0

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US-10-667-289-2 (1-629) x US-10-667-290-1 (1-2859)

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Qy      1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
Db      119 ATGATCAKGTCACTATTCAATGGATGCGATATAGCCCTTTACATCTCTCACTGG 178
Qy      21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGlnProIleThr 40
Db      179 TGCATGAGAGATTAACAATATTAATTAATGCTCTGGCCACATCTGGGTAGAAACAGCCACA 238
Qy      41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
Db      239 ATTTTAAAGTGGGTATGAAATATCTCATATATTTGCCAACACCAATTAAGAACTGCCAA 298
Qy      61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGlnLubArgPheGlnIleThrArgIle 80
Db      299 CGAAGGAACCTTCAATTTTATTAATAATGGCATCAAGAAAGATTTCAATACACAGGATT 358
Qy      81 AsnLysThrThrAlaArgLeuTrpTyrLysAsnPheLeuGlnProHisAlaSerMetTyr 100
Db      359 AATTAACCAACACACTGGCTTGTGTATTAATAAATCTTCTGGAACACATGCTTCTATGTAC 418
Qy      101 CysThrAlaGlnCysProLysHisPheGlnGlnThrLeuIleCysGlyLysAspIleSer 120
Db      419 TGCACGTGTAATGTCCCAACATTTTCAAGACACCTGATATGTGGAAAAACATTTCT 478
Qy      121 SerGlyTyrProProAspIleProAspGlnValThrCysValIleTyrGlyTyrSerGly 140
Db      479 TCTGATATCCGCCAGATATTTCTGATGAAGTAACTGTGTCTATTTATGAAATTTCAAGCC 538

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QY 141 AsnMetThrCysThrTrpAsnAla**LysLeuThrTyrIleAspThrIleValVal 160
 DB 539 AAcATGACTTGACCTCGAATGCTRGAGAGCTCACTACATAGACAAATAATAGTGTGA 598
 QY 161 HisValLysSerLeuGluThrGluGluGlnGlnIleuThrLeuThrSerSerTyrIleAsn 180
 DB 599 CATGTGAAGAGTTAGAGACAGAAAGAGCAACAGATCTCACTCAAGGTATATTAAC 658
 QY 181 LLeSerThrAspSerLeuGlnGlyLysLeuThrValTrpValGlnAlaAsn 200
 DB 659 ATCTCCACTGATTCATTAACAAGTGGCAAGAGTACTGTGGGTCCAGACGCAAC 718
 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
 DB 719 GCATAGGCACTGAAAGAGTCAAAACACTGCAATTCACCTGATGATATAGTATACCT 778
 QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIle 240
 DB 779 TCTGACAGCCGATTCCTCAGGGCTGAGACTATTAATCTACAGTCCCAAGACCATAT 838
 QY 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
 DB 839 TATTGGATAGTCAACAACAAATTGAAAGGTTCTGTGAATGAGATVCAAGGCTTACA 898
 QY 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAspPheThrTyrValGlnGlnSer 280
 DB 899 ACAACCAAACTTGAGATTTAAAGATTTGACACCAATTTACATATGTCGAACACTCA 958
 QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
 DB 959 GAATTCACCTTGAGCCAAACATTAAGTACGTATTCAGATGAGATGTCAAGAAACAGGC 1018
 QY 301 LysArgTyrTrpGlnProTyrPheSerProPhePheHisTyrThrProGluThrValPro 320
 DB 1019 AAAAGGTACTGGCAGCCTTGAGTCACTCTTTTATTAATAACCTCGAAACGTTCCC 1078
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
 DB 1079 CAGGTCACTCAAAAGATTCCAACATGACATGATGATTCGGGCTTACAGTTGCTTCC 1138
 QY 341 LLeSerThrGlyHisLeuThrSerAspAsnArgLysAspIleGlyLeuLeuLeuGlyMet 360
 DB 1139 ATCTCTACAGGAGCCTTACTTCTGACACAGAGAGACATTTGATTTATGGGAATG 1198
 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
 DB 1199 ATGCTCTTCTGTATGTGTCAATTCCTTCTTGTGAGATTAATTAAACAGATCAATTC 1258
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
 DB 1259 CGAATCGGATTTAAAGAGAGATCTTATTTTANTACCAAGTGGCTTTATGAGATATTT 1318
 QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLysAsnSerGluLeuMetAsn 420
 DB 1319 CTTAATATGAAAAACAGCAATGTGTCAAAATGTCAAGAAAAATAGTGAATTAATGAT 1378
 QY 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440
 DB 1379 AATTAATTCAGTGAAGGTCTTAATAGTTGATCCCTGATTCAGAGATAAAAGAAATC 1438
 QY 441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
 DB 1439 TTCAATCCAGAAACAGAGCTTACAGACTTACAGAGAGAGATACAGAACCCCTGGAGACA 1498
 QY 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
 DB 1499 AGAGACTACCCGAAAACTCGTATTCGACATATCTACATGTATATATTCCTGATCTC 1558
 QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500
 DB 1559 AACACGTGATATTAACCCCAAAATTTCTGCTTGAAGGAAACCATTCACAGCAAT 1618
 QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520

DB 1619 AATPATGAATTAATCTTCCTTAACACTTAAACCAACCACTGATCTTACAGTCAAGAAAT 1678
 QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
 DB 1679 AATCCAGGTGTACAAAAGCAATCCTAATTTGCTTTTCTGTTCAGAGTGAATTCCTA 1738
 QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyGluCysSerSer 560
 DB 1739 AGCAACCAATATTTCTTGAGAGATTAAGCTCATATTAATCAAGAGAGATGCAATTCCT 1798
 QY 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
 DB 1799 CCGACATCAAAACACTCAGTAGAGAGAGAAACCAACCATGCTTTTGAATAATGATTCACCC 1858
 QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
 DB 1859 AGTGAACATATTCACAGAAACAGACCCTGCTTCGTATGTAATTTGCTCTGTTGGGATC 1918
 QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGluAsnIleLeuGluSerHis 620
 DB 1919 GTGAAATGAGAGTTGCCATCTTATTAATCTTATTTTCCAAATAATTTTGGAAAGCAC 1978
 QY 621 PheAsnArgLysSerLeuLeuGlyLys 629
 DB 1979 TTCAATAGATTCACCTTGAAAG 2005
 RESULT 6
 US-09-972-708-20
 ; Sequence 20, Application US/09972708
 ; Publication No. US20030059871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; APPLICANT: Cosman, David J.
 ; APPLICANT: Mosley, Bruce A.
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Dubose, Robert F.
 ; APPLICANT: Wiley, Steven R.
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
 ; FILE REFERENCE: 3160-B
 ; CURRENT APPLICATION NUMBER: US/09/972,708
 ; CURRENT FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 1890
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-972-708-20
 Alignment Scores:
 Pred. No.: 0 Length: 1890
 Score: 3314.00 Matches: 626
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 3
 Query Match: 99.6% Indels: 0
 Gaps: 0
 US-10-667-289-2 (1-629) x US-09-972-708-20 (1-1890)
 QY 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
 DB 1 ATAAATCAGGTCACTTATTCATATGAGATGCAGTAAATAGCCCTTTTACATCTTCACTG 60
 QY 21 CysHieGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
 DB 61 TGTCAATGAGAGATTCATAATATATACTGCTCGCCACATCTCGGGTAGAACAGCCACA 120
 QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
 DB 121 ATTTTAAAGTGGATGTAATATCTCTATATATTTGCAACAGACAAATTAAGAACTGCAA 180
 QY 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluLysArgPheGlnIleThrArgIle 80

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Db      181  CCAAGGAACTTCATTTTATAAAAAATGCGATCAAAAGATTTCACACAGATT 240
Qy      81  AsnLysThrThrAlaArgLeuTrpTyrLysAsnPhelLeuGluProHisAlaSerMetTyr 100
Db      241  AATTAACACACAGCTGGCTTTGGATTAATAAACTTTTGAACCAATGGCTTATATAC 300
Qy      101  CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
Db      301  TGACCTGCTGAATGTCCTCAAAATTTTCAAGAGACACATGATATGTGAAAAAGACATTCT 360
Qy      121  SerGlyTyrProPheAspIleProAspGluValThrCysValIleIleTyrGlyTyrSerGly 140
Db      361  TCGGATATCCGCGCAAGATATTCGATGAAGTAACTGGTCATTTATGATATATTCAGGC 420
Qy      141  AsnMetThrCysThrTPAsnAla**LysLeuThrTyrIleAspThrLysTyrValVal 160
Db      421  AACATGACTTGACCTGGAATGCTGGAGAGCTCACTCATATGACACAAATATCGTGTAT 480
Qy      161  HisValLysSerLeuGluThrGluGluGluGlnIleThrLeuThrSerSerTyrIleAsn 180
Db      481  CATGTGAAGAGTTTAAAGACAGAAAGAGCAAGATATCTCACTCAAGCTATATTAAC 540
Qy      181  IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGlnAlaAlaAsn 200
Db      541  ATCTCCACTGATTCATTACAAAGGTGCGAAGAGTAACTGGTTGGTCCAAAGCAAGAAC 600
Qy      201  AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
Db      601  GCATCAGCATGAGAGAGTCAAAACAACTGCATTCACCTGAGATGATATGATATCT 660
Qy      221  SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db      661  TCTGCAACCCGCTCATTTCCAGGGCTGAGACTTAATATCTACAGGCCCAAGACCATAT 720
Qy      241  TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetAlaGlyTyrValAlaThr 260
Db      721  TATGGGATATGTCAAACAAACATTTGAAAGGTTTCTGTGTAAGAAAGATTCAGAGCTTACA 780
Qy      261  ThrAsnGlnThrTPAsnValLysGluPheAspThrAsnPhetTyrValGlnGluSer 280
Db      781  ACNAAACCAACTTGGAATGTTAAAGAAATTTGACCCAAATTTTACATATGTCACAGTCA 840
Qy      281  GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db      841  GAATTTCTACTTGAGCCAAACATTAAGTACGTATTTCAAGTGAATGTCAGAAACAGGC 900
Qy      301  LysArgTyrTrpGlnProTyrPheSerProPhePheHisLysThrProGluThrValPro 320
Db      901  AAAAGGTACTGGCAGCCCTTGAGTTCCTGTTTTTTCATAAAACACCTGAAACAGTCC 960
Qy      321  GlnValThrSerLysAlaPheGlnHisAspThrTPAsnSerGlyLeuThrValAlaSer 340
Db      961  CAGATCACAATAAAGCATTCACATGACATGACATGAAATTTGGGCTTACAGTTGCTTCC 1020
Qy      341  IleSerThrGlyHisLeuThrSerAspAsnArgLysAspIleGlyLeuLeuLeuGlyMet 360
Db      1021  ATCTCTACAGGGCAGCTTACTTCTGACAAACAGAGAGCATTTGAGCTTTATTTGGGATG 1080
Qy      361  IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db      1081  ATCTCTTTGCTGTTATGTTGTCAATCTTCTTGTGATGGATATTTAAACAGATCATTC 1140
Qy      381  ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrPheLysGluAspIle 400
Db      1141  CGAACTGGAGTTTAAAGAGAGATCTTATTTTAAATCCAAAGTGGCTTTATGAAGATTT 1200
Qy      401  ProAsnMetLysAsnSerAsnValValLysMetLeuGlnIleAsnSerGluLeuMetAsn 420
Db      1201  CCTATATGAAAAACAGCAATGTTGTGAATAATGTCAAGAAATATGAGATTAATGAT 1260
Qy      421  AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440

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Db      1261  AATTAATTCAGTAGCAGCTCTTATATGTTGATCCCATGATTAACAGATTAAGAAATC 1320
Qy      441  PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
Db      1321  TTGATCCCGAACAACAAGCTTACAGACTACAAAGAGAGATACAGAGACCCCTGGAGACA 1380
Qy      461  ArgAspTyrProGluAsnSerLeuPheAspThrThrValValTyrIleProAspLeu 480
Db      1381  AGAGACTACCCGCAAAATCTGCTATTCGACAAATACACATGATATATATATCTGATCTC 1440
Qy      481  AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500
Db      1441  AACATGGAATTAATTAACCCCAATTTTCAAAATTTTCTGCTAGAGGAGAACCTTCAGCAT 1500
Qy      501  AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db      1501  AATTAATGAATTAATCTTCTTAACCATTAACCAAGCAAGTATCTTATGACTCAGGAAAT 1560
Qy      521  AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db      1561  AATCCCAAGTTTACAAAGCATCTTAATTTGCTTTTCTGTTCAAGTGTGAATTCCTA 1620
Qy      541  SerAsnThrIlePheLeuGluGluLysSerLeuIleLeuAsnGlnGluCysSerSer 560
Db      1621  AGCAACACAAATATTTCTTGAAGAAATTAAGCTCATATTAATCAAGAGAAATGCAATTC 1680
Qy      561  ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
Db      1681  CTGACATACAAAACTCAGTAAAGAGAGAGAAACCAACCATGCTTTTGGAAAAATGATTCACC 1740
Qy      581  SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db      1741  AGTGAACATAATTCAGAAACAGACCCTGCTTCGATGAATTTTCTCTCTTTGGGGATC 1800
Qy      601  ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
Db      1801  GTGAATGAGAGGTGGCCATCTATTAATCTTAATTTTCCAAATAATTTTGGAAAGCCAC 1860
Qy      621  PheAsnArgIleSerLeuLeuGluLys 629
Db      1861  TTCAATAGATTTTCACTCTTGAAAG 1887

RESULT 7
US-10-715-667-20
; Sequence 20, Application US/10715667
; Publication No. US20040152161A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OR INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-715-667-20

Alignment Scores:
Pred. No.: 0
Score: 3314.00
Percent Similarity: 99.5%
Best Local Similarity: 99.5%
Query Match: 99.6%
Length: 1890
Matches: 626
Conservative: 0
Mismatch: 3
Indels: 0

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DB: 8 Caps: 0

US-10-667-289-2 (1-629) x US-10-715-667-20 (1-1890)

QY 1 MetAsn***ValThrIleGlnTPAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20

DB 1 ATGAATCAGGTCACCTATTCATAGGAGTACAGTAATAGCCCTTATACATACCTTCAGCTGG 60

QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40

DB 61 TGTCAATGAGAAATATACAAATATATAATGCTCTGGCCACATCTGGAGTAAACCAAGCCACA 120

QY 41 IlePheIleMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLeuAsnCysGln 60

DB 121 ATTTTATAGATGGGTATGAAATATCTCTATATATTTGCCACAGCAATTAAGAACTGCCAA 180

QY 61 ProArgLeuLeuHisPheTyrLeuAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80

DB 181 CCAAGGAACTTCATTTTATATAAAATGCGATCAAAAGAAATTTCAATTCACAAAGATT 240

QY 81 AsnLeuThrThrAlaArgLeuTyrTyrLeuAsnPheLeuGluProHisAlaSerMetTyr 100

DB 241 AATTAACCAACACACTCGCTGGTATTAATAAACTTCTTGGAACCACTGCTTCTATGTAC 300

QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLeuAspIleSer 120

DB 301 TGCATCTGCTAAATGTCCTCAACATTTTCAAGACACTGATATGTGAAAAGACATTTCT 360

QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140

DB 361 TCTGGAATCTCGGCAAGATATTCCTGATGAAGTAACTGTCATTTATGATATTCAGGC 420

QY 141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTyrIleAspThrLysTyrValVal 160

DB 421 AATCATGCTTGCACTGGAATGCTGGAGACCTCACTCAATAGACAAATAATCTGTGTA 480

QY 161 HisValLysSerLeuGluThrGluGluGlnGluIleThrLeuPhePheSerTyrIleAsn 180

DB 481 CATGTGAAGGTTTAGAGACAGAAAGACAAACAGATCTCACTCAAGCTATATTTAAC 540

QY 181 IleSerThrAspSerLeuGlnGlyLysLeuTyrLeuValTrpValGlnAlaAlaAsn 200

DB 541 ATCTCCACTGATTCATTAACAAGGTGCAAGAAAGTACTGTTGGGTCCAAAGACGCAAC 600

QY 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220

DB 601 GCACTAGGCAATGAGAGTCAAAACCACTCAATTCACCTGATGATATAGATGATCTCT 660

QY 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240

DB 661 TCTGCAAGCCGTCATTTCCAGAGGCTGAGACTATTAATCTCAAGTGCACCAAGACCATTAAT 720

QY 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260

DB 721 TATTTGGATAGTCAAAACAACATTGAAAGTTTCCGTGTAATAGATATCAAGGCTACA 780

QY 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280

DB 781 ACAAAACCAAACTTGAAATGTTTAAAGAAATTTGACCAAAATTTTACATATGTGCAACAGTCA 840

QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300

DB 841 GAATTTCACTTGAGCCAAACATTAAAGTACGATTTTAAAGTACGATTCAGAAACAGGC 900

QY 301 LysArgTyrTrpGlnProTyrPheSerProPhePheHisLeuSerThrProGluThrValPro 320

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QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340

DB 961 CAGGTCAATCAAAAGCAATTCACATGACACAAAGAAATTCCTGGGCTTAAACAGTTGCTTCC 1020

QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360

DB 1021 ATCTTACAGGCACTTACTTCTGACAAACAGAGACACTTGGACTTTATTTGGGAATG 1080

QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380

DB 1081 ATGCTCTTGGCTGTATGTTGTCAAATCTTCTTTGATTTGGGATATTTAAACAGATCAATTC 1140

QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400

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DB 1321 TTCTATCCAGACACAAAGCTTACAGACTACAAAGAGAAATACAGAACCCCTGAGACA 1380

QY 461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480

DB 1381 AGAGACTACCCGCAAACTGCTATTCGACAAATACTACAGTGTATATATTCCTGATCTC 1440

QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluLysSerHisLeuSerAsn 500

DB 1441 AACACTGGAATATAACCCCAAAATTTCAAAATTTCTCTGAGGAGAAAGCCATTCAGCAAT 1500

QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520

DB 1501 AATTAATGAATTAATCTTCTTACACTTAACCAACAGTTCATTTCTTAGCTCAGGAAT 1560

QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540

DB 1561 AATCCAGGTTACAAAGACATCTAATTTTGGCTTTCTGTTCAAGTGTGAATTCACCTA 1620

QY 541 SerAsnThrIlePheLeuGlyLysLeuSerLeuIleLeuAsnGlnGlyLysCysSerSer 560

DB 1621 AGCAACACATATATTTCTTGAGAAATTAAGCTCATATTAATCAAGAGAAATCAAGTTCT 1680

QY 561 ProAspIleGlnAsnSerValGluGluThrThrMetLeuLeuAsnAspSerPro 580

DB 1681 CCGACATCAAAACTCAGTAGAGAGAGAAACCACTGCTTTTGGAAATGATTCACCC 1740

QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600

DB 1741 AGTGAACATATTCAGAAACAGACCTGCTTCCAGATGAATTTGCTCTTTGGGGATC 1800

QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620

DB 1801 GTGAATGAGAGATGTCATCTATTAATTAATTTTCCAAAAATATTTTGGAAAGCCAC 1860

QY 621 PheAsnArgIleSerLeuGluLys 629

DB 1861 TTCATATGAGATTCACCTTGGAAAG 1887

RESULT 8

US-10-105-930-9

; Sequence 9, Application US/10105930

; Publication No. US20030009018A1

; GENERAL INFORMATION:

; APPLICANT: Maeda, Masateugu

; APPLICANT: Yasuchi, No. US20030009018A1ko

; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12

; FILE REFERENCE: 06501-105U51

; CURRENT APPLICATION NUMBER: US/10/105, 930

; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER: PCT/JP00/06654

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: JP 2000-240397


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Db      1801 GTGATGAGAGGATTCATCTATTAACTATTTCACAAAATATTTGGAAAGCCAC 1860
Qy      621 PheAsnArgIleSerLeuLeuGluLys 629
      |||
Db      1861 TTCAATAGGATTTCACTCTTGGAAAG 1887

RESULT 9
US-09-972-708-19
; Sequence 19, Application US/09972708
; Publication No. US20030059871A1
;
GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-19

Alignment Scores:
Pred. No.:      0      Length:      2830
Score:          3314.00  Matches:      626
Percent Similarity: 99.5%  Conservative: 0
Best Local Similarity: 99.5%  Mismatches: 3
Query Match:      99.6%  Indels:      0
DB:               3      Gaps:      0

US-10-667-289-2 (1-629) x US-09-972-708-19 (1-2830)
Qy      1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
      |||
Db      107 ATGATAGAGGTCACTATTTCATAGGATGAGATGACAGTAATACCCCTTTACATACCTTCAGCTGG 166
Qy      21 CysHieGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
      |||
Db      167 TGCATGAGAGGATTAACAATATAAATGCTGCTGGCCACATCGGTAAGAACGCCACA 226
Qy      41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
      |||
Db      227 ATTTTAAAGTGGGTATGATATCTCTATATATGGCCAGAGCAATTAAGAACTGGCAA 286
Qy      61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
      |||
Db      287 CCAAGGAAACTTCATTTTATAAATAATGGCATCAAAAGAAAGATTCCAATCAACAAGGATT 346
Qy      81 AsnLysThrThrAlaArgLeuTrpTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
      |||
Db      347 AATTAACAACAAGCTGGCTTGGTATTAATAAATCTTTCGAACAACATGCTTCATATAC 406
Qy      101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
      |||
Db      407 TGCACGCTGTAATGTCCTCCAAACATTTTCAGAGACACATGATATGGAAAAAGACATTTCT 466
Qy      121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
      |||
Db      467 TCTGGATATCCGACAGATATCTCGATGAAGTAACCTGTGCATTTATGAAATATTCGGCC 526
Qy      141 AsnMetThrCysThrTrpAsnAla**LysLeuThrTyrIleAspThrLysTyrValVal 160
      |||
Db      527 AACATGACTTGCACTGGAATGCTGGGAAGCTCACCTACATAGACAAATACGTGTA 586
Qy      161 HisValLysSerLeuGluThrGluGluGlnGlnIleTyrLeuThrSerSerTyrIleAsn 180
      |||

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Db      587 CATGTGAAGATTAGAGACAGAAAGAACAGATATCTCACTCAAGCTATATTAAAC 646
Qy      181 IleSerThrAspSerLeuGlnGlyLysLysTyrIleValIleTrpValGlnAlaAlaAsn 200
      |||
Db      647 ATCTCCACTGATTCATTACAGAGGTGGCAAGAGATCTTGTTGGGTCCAGACGCCAAC 706
Qy      201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisAlaLeuAspIleValIlePro 220
      |||
Db      707 GCACTAGGATGGAAGATGCAAAACACATCAATTCACCTGGATGATATAGTATACCT 766
Qy      221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
      |||
Db      767 TCTGACGCCGTCAATTTCCAGGCGCTGACACTATAAATCTACAGGCCCAAGACCATTAAT 826
Qy      241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
      |||
Db      827 TATTTGGATAGTCAAACACAAATTTGAAAGGTTTCTGTGAATAGATACAGGCTTACA 886
Qy      261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
      |||
Db      887 ACAAACCAACTGGATGTAAAGATTTGACACCAATTTTACATATGTCACACAGTCA 946
Qy      281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
      |||
Db      947 GAATTCATCTTGAGGCCAAACATTAAGTACGTATTTCAAGTGAAGATGCAAGAAACAGGC 1006
Qy      301 LysArgTyrTrpGlnProTrpSerSerProPhePheHisLysThrProGluThrValPro 320
      |||
Db      1007 AAAAGTACTGGCAGCCTTGAGTTCACGTGTTTTTATTAACACCTGAAACGTTCC 1066
Qy      321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
      |||
Db      1067 CAGGTCACTCAAAAGATTCCAACATGACACATGGAATCTGGGCTTAACAGTCTTCC 1126
Qy      341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
      |||
Db      1127 ATCTCTACAGGCACTTACTTCTGACACAGAGAGACATTTGACATTTATTTGGGATG 1186
Qy      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
      |||
Db      1187 ATGCTCTTGTCTGTATGTTGTCAAATCTTTCTTGTGATGGATATTAAACAGATCAATTC 1246
Qy      381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
      |||
Db      1247 CGAATCGGATTTAAAGAAAGATCTTATTTTAATACCAAGTGGCTTTATGAAGATATT 1306
Qy      401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420
      |||
Db      1307 CTTAATATGAAAAACAGCAATGTTGTGAATAATGCTACAGGAAATAGTGAATATGAAAT 1366
Qy      421 AsnAsnSerSerGluGlnValIleTyrValAspProMetIleThrGluIleLysGluIle 440
      |||
Db      1367 AATTAATTCAGTAGCAGCGCTTATATGTTGATCCCATGATTCACAGAGTAATAAGAAATC 1426
Qy      441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
      |||
Db      1427 TTCAATCCAGAACACAGAGCTTACAGACTACAGAGAGAGAAATACAGAACCCCTGGAGACA 1486
Qy      461 ArgAspTyrProGluAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
      |||
Db      1487 AGAGACTACCCGCAAACTGCTATTCGACAAATACTACAGTTATATATCTCGATCTC 1546
Qy      481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluLysSerHisLeuSerAsn 500
      |||
Db      1547 AACACTGGATATTAACCCCAATTTTCGATCTGCTGAGGAGAACCATTCACAGCAAT 1606
Qy      501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
      |||
Db      1607 AATATAGAAATTAATCTTCACTTAACATTTAAACCAACGAGTTGATCTTAGACTCAGGAAT 1666
Qy      521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
      |||
Db      1667 AATCCAGGTTACAAAGACATCTTAATTTGTCTTTTCTGTTCAGATGGAATTCACCTA 1726

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Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerIleuIleuAsnGlnGlyGluCysSerSer 560
Db 1727 AGCAACACAAATATTTCTTGAGAAATTAAGCTCATATTAATCAAGAGATGAGTTCT 1786
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
Db 1787 CCTGACATTAACAACTAGTAGAGAGAGAAACCAACATGCTTTGGAAAAATGATTCACCC 1846
Qy 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1847 AGTGAAACATTCAGAAACAGACCCCTGCTTCGATGATTAATTCCTCTGTTGGGATC 1906
Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrrPheProGlnAsnIleLeuGluSerHis 620
Db 1907 GTGAATGAGAGGTGCATCATTAATTAATTTTCCAAATAATTTGGAAAGCCAC 1966
Qy 621 PheAsnArgIleSerLeuLeuGluLys 629
Db 1967 TTCATAGATTTCATCTTGAAAG 1993

RESULT 10

US-10-715-667-19
Sequence 19, Application US/10715667
Publication No. US20040152161A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cozman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/10/715,667
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/09/972,708
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 2830
TYPE: DNA
ORGANISM: Homo sapiens
US-10-715-667-19

Alignment Scores:

Pred. No.: 0 Length: 2830
Score: 3314.00 Matches: 626
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 3
Query Match: 99.6% Indels: 0
DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-10-715-667-19 (1-2830)

Qy 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrrIleLeuPheSerTrp 20
Db 107 ATGAATCAGGCTACTATTCATAGGAGTGCAGTAATTAAGCCCTTTCATACATCTTCAGCTGG 166
Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
Db 167 TGTCATGAGAAATTACAAATATATTAACGCTGCGCAATCTGGTAGAACCCAGCA 226
Qy 41 IlePheIleMetGlyMetAsnIleSerIleTyrrCysGlnAlaAlaIleValAsnCysGln 60
Db 227 ATTTTAAGAGGGTATGAATATCTCTATATATGCGAAGAGCAATTAAGAACTGCGCA 286
Qy 61 ProArgIleLeuHisPheTyrrIleAsnGlyIleIleGluArgPheGlnIleThrArgIle 80
Db 287 CCAAGGAAATCTCTTTTATTAATAAATGCGATCAAGAAAGATTTCAAATCAAGAGATT 346
Qy 81 AsnIleThrThrAlaArgLeuTrpTyrrIleAsnIleLeuGluProHisAlaSerMetTyrr 100

Db 347 AATAAACAAACACTGGCTTTGGTATAAAAACCTTCTGGAACCACTGCTTATGATAC 406
Qy 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
Db 407 TGCATCTGTAATCTCCCAACATTTTCAAGAGACCTGATATGTGAAAAAGCATTTCT 466
Qy 121 SerGlyTyrrProProAspIleProAspGluValThrCysValIleTyrrGluTyrrSerGly 140
Db 467 TCTGGATATCCGCAATATCTCGATGAAGTAACCTGTGTCTATTAATATTCAGGC 526
Qy 141 AsnMetThrCysThrTrpPheAla***LysLeuThrTyrrIleAspHisLysTyrrValVal 160
Db 527 AACATGACTTGCACTGGAAATGCTGGAACTCACTACATTAACCAAAATATCGTGA 586
Qy 161 HisValIleSerLeuGluThrGluGluGlnGlnIleTyrrLeuThrSerSerTyrrIleAsn 180
Db 587 CATGTAGAGGTTTAGAGACAGAGAGAGCAACAGATATTCACCTCAAGCTATATTAC 646
Qy 181 IleSerThrAspSerLeuGlnGlyLysLysTyrrLeuValTrpValGlnAlaAlaAsn 200
Db 647 ATCTCCACTGATTCATTACAAGGTGGCAAGAGTACTGTGGTTGGGCCAAGCAGCAAC 706
Qy 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisIleuAsnAspIleValIlePro 220
Db 707 GCACTAGGCAATGGAAGGTCAAAACATGCAAAATTCACCTGATGATATAGATGATCCT 766
Qy 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db 767 TCTGCAAGCCCTCATTTTCCAGGCTGAGACATTAATATCTCACTGCGCAAGACATATT 826
Qy 241 TyrrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrrLysAlaThr 260
Db 827 TATTTGGATGTGCAACCAATTTGAAGAGTTCCGTGTAATGTAGATCAAGGCTACA 886
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrrValGlnIleSer 280
Db 887 ACAACCAAACTTGAAATGTTAAAGAAATTTGAACCAATTTTCAATATGTGCAACAGTCA 946
Qy 281 GluPheTyrrLeuGluProAsnIleLysTyrrValPheGlnValArgCysGlnGluThrGly 300
Db 947 GAATTCCTACTGAGCCCAACATTAAGTACGTATTTCAAGTGAAGATCAAGAAACAGGC 1006
Qy 301 LysArgTyrrTrpGlnProTrpSerSerProPheHisLysThrProGluThrValPro 320
Db 1007 AAAAGTACTGGACCTTGAGTTCACTGTTTTCATTAACACCTGAAACAGTTCCC 1066
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db 1067 CAGGTCAATCAAAAGCAATTCAAACATGACACATGGAATTTGAGCTTAACAGTTGCTTC 1126
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
Db 1127 ATCTCTACAGGCACTTACTTCTTGACACAGAGAGACCTTGAATTTATTTGGGAATG 1186
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1187 ATCGTCTTCTGTATGTTGTCAATCTTCTTTGATGGATATTAACATCATTC 1246
Qy 381 ArgThrGlyIleLysArgAlaGlyIleLeuLeuIleProLysTrpLeuTyrrGluAspIle 400
Db 1247 CGAACTGGAGTTAAAGAAAGATCTTAATGTATATCAAAAGTGGCTTAATGAAGATATT 1306
Qy 401 ProAsnMetLysAsnSerAsnValAlaLysMetLeuGlnGluAsnSerGluLeuMetAsn 420
Db 1307 CTTAATATGAAAAACAGCAATGTTGTGAAAAATCTACAGAAAAATAGTAATTAAT 1366
Qy 421 AsnAsnSerSerGluGlnValLeuTyrrValAspProMetIleThrGluIleLysGluIle 440
Db 1367 AATATATCCAGTAGAGGTCTATATAGTTGATCCCATGTATCAGAGATAAAGAAATC 1426
Qy 441 PheIleProGluHisLysProThrAspTyrrLysLysGluAsnThrGlyProLeuGluThr 460

Db 1427 TTCATCCAGAACAAAGCCTTACAGACTACAAAGAGGAAATACAGAGACCCCTTGAGACA 1486
Qy 461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrVal1Val1TyrIleProAspLeu 480
Db 1487 AGAAGTACCCGCAAACTCGCTATTCAGCAATACACTACAGTTGATATATTCCTGATCTC 1546
Qy 481 AsnThrGlyTyrIleProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500
Db 1547 AACCTGATATTAACCCCAATTTCAATTTTCTGCTGAGGAGACGACATCAGCAAT 1606
Qy 501 AsnAsnGluIleThrSerLeuThrLeuIleProProValAspSerLeuAspSerGlyAsn 520
Db 1607 AATATGAAATTAATCTTCCTTAACCTTAACCAACAGATGATTCCTTAAGCTCAGAAAT 1666
Qy 521 AspProGluLeuGlnIlePheProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db 1667 AATCCAGGTATCAAAAGCATCTTAATTTGCTTTCTGTTCAAGGTGAATTCACATA 1726
Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnIleGluCysSerSer 560
Db 1727 AGCAACACANATTTCTTGAGATTAAGCTCATATTAATCAAGGAGATGACATTCCT 1786
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
Db 1787 CCTGACATACAAACTCAGTACAGAGAAACCAACATGCTTTGGAAAATGATTCACACC 1846
Qy 581 SerGluThrIleProGluGlnIleThrLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1847 AGTAAACTATTCAGAAACAGACCCCTGCTTCATGATGAATTTGCTCCTGTTGGAGATC 1906
Qy 601 ValAsnGluLeuLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
Db 1907 GTGATATGAGAGTTGCCATCATTAATTAATTTTCCACAAATATTTTGGAAAGCCAC 1966
Qy 621 PheAsnArgIleSerLeuLeuGluLys 629
Db 1967 TTCATATGATTTCACTCTTGAAAG 1993

RESULT 11
US-10-105-930-5
; Sequence 5, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OR INVENTION: NOVEL HEMOPOLYMERIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT FILING DATE: US/10/105, 930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98) ... (1984)
US-10-105-930-5

Alignment Scores:
Pred. No.: 0 Length: 2123
Score: 3292.00 Matches: 622
Percent Similarity: 99.2% Conservative: 2
Best Local Similarity: 98.9% Mismatches: 5
Query Match: 99.0% Indels: 0
DB: 6 Gaps: 0

US-10-667-289-2 (1-629) x US-10-105-930-5 (1-2123)
Qy 1 MetAsn***ValThrIleGlnIleProAspAlaValIleAlaLeuTyrIleLeuPheSerTyr 20
Db 98 ATGATCAGGTCACTATTCATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 157
Qy 21 CysHisGlyIleIleThrAsnIleAsnCysSerGlyHisIleTyrPheValGluProAlaThr 40
Db 158 TGTCTATGAGAGATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 217
Qy 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
Db 218 ATTTTAAATGAGGTGATGATATCTCATATATATGCAACAGCAATTAAGAACTGCCAA 277
Qy 61 ProArgLysLeuHisPheTyrIleAsnGlyIleLysGluThrPheGlnIleThrArgIle 80
Db 278 CCAAGGAACCTTCAATTTTAAATAATGATCAAAAGAAAGATTTCAAATCAAGAAATTT 337
Qy 81 AsnLysThrThrAlaArgLeuTyrTyrIleAsnPheLeuGluProHisAlaSerMetTyr 100
Db 338 AATTAACAAACACCTCGCTTGTGTATTAATACTTCTGGAACCAACATGCTTCTATATGAC 397
Qy 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyIleAspIleSer 120
Db 398 TGCACCTGTAATGTCCTCAAAACATTTTCAAGAGACACTGATATGAGAAAAGACATTTCT 457
Qy 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
Db 458 TCTGATATCCGACAGATATTCCTGATGAGATTAACCTGTCTCATTTATGAAATATTCAG 517
Qy 141 AsnMetThrCysThrTyrPheAlaIle***LysLeuThrTyrIleAspThrLysTyrValIle 160
Db 518 AACATGACTTGCACTGGAATGCTGGAGGCTCACTCAATAGACAAATACAGTGTGTA 577
Qy 161 HisValLysSerLeuGluThrGluGluGlnGlnIleThrLeuThrSerSerTyrIleAsn 180
Db 578 CATGTGAAGATTTAAGACAGAAAGAGCAACAGATATCTCACTCACTCACTATATTAAC 637
Qy 181 IleSerThrAspSerLeuGlnGlyIleLysLysTyrLeuValTyrPheValGlnAlaAsn 200
Db 638 ATCTCCACTGATTCATTAACAGGTGCGAAGAGAAAGTATGTTGGTCCAGACGCAAC 697
Qy 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisIleAsnAspAlaIleValIlePro 220
Db 698 GCATAGGACATGGAAGATCAAAACATCTCAAAATTCACCTGATGATATATGATATCTT 757
Qy 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db 758 TCTGACGCCGTCATTTCCAGGGCTGAGACTATAATGCTACAGTGCACAGACCATATAT 817
Qy 241 TyrTyrAspSerGlnThrIleGluLysValSerCysGluMetCysGlyTyrValAlaThr 260
Db 818 TATTTGGATATGTCAAACAAATTTGAAGATTTCCGTGTAATATGAGATTCAGAGCTACA 877
Qy 261 ThrAsnGlnThrTyrAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
Db 878 ACAAAACCAACTTGAAATGTTAAAGATTTGACACCAATTTTACATATATGCAACATCA 937
Qy 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db 938 GAATTCATCTTGAGCCCAACATTAAGTACGTATTTCAAGTGAATGTCAGAAACAGGC 997
Qy 301 LysArgTyrTyrGlnProTyrPheSerProPhePheHisLysThrProGluThrValPro 320
Db 998 AAAAGTACTGCGACCTTGAGTTCACTGTTTTTTCATTAACCACTGAACAGTTCCC 1057
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTyrAsnSerGlyLeuThrValAlaSer 340
Db 1058 CAGGTCACTCAAAAGATTCCAACATGACATGCAATTCAGGCTCAACAGTTGCTTCC 1117
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgLysAspIleGlyLeuLeuGlyMet 360

Db 1118 ATCTTACAGGGACCTTACTTGTGACACAGAGACATTTGACTTTTATTTGGGAATG 1177
Qy 361 ILeValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1178 ATGCTCTTGTCTGTATGTTGTGCAATCTTTCTTTGATTTGGACATTTAACATCTATTC 1237
Qy 381 ArgThrGlyIleLeuValArgArgIleLeuLeuLeuIleProlySerPleuTyrgluAspIle 400
Db 1238 CGAACTGGAGTTAAAGAGATCTTATTTGTTAATCAAAAGTGGCTTTATGAAATATT 1297
Qy 401 ProAsnMetIysAsnSerAsnValValIleMetLeuGlnGluAsnSerGluLeuMetAsn 420
Db 1298 CCTATATGAAAAACACCAATGTTGTAATAATGCTACAGAAATAGTGAATATATAAT 1357
Qy 421 AsnAsnSerSerGluGlnValLeuTyValAspProMetIleThrGluIleGlyIle 440
Db 1358 AATTAATTCAGTGGAGCGCTCTATATGTTGATTCCTGATTCAGAGATTAAGAAATC 1417
Qy 441 PheIleProGluIleIleValProThrAspTyrglyIleGluAsnThrGlyProLeuGluThr 460
Db 1418 TTCTATCCAGAACACCAAGCCTACAGACTACAGAGAGAAATACAGACCCCTGAGACA 1477
Qy 461 ArgAspTyrglyProGluAsnSerLeuPheAspAsnThrThrValValTyrglyIleProAspLeu 480
Db 1478 AGAGACTACCCGCAAACTGCTATTTGACAAATACACAGTTGATATATTCCTGATCTC 1537
Qy 481 AsnThrGlyTyrglyProGluIleSerAsnPheLeuProGluGlySerHisIleSerAsn 500
Db 1538 AACCTGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAACCATCTCATATAT 1597
Qy 501 AsnAsnGluIleThrSerLeuThrLeuIleProProValAspSerLeuAspSerGlyAsn 520
Db 1598 AATTAATGAATTAATCTTCTTAACACTTAACCAACAGTTGATCTTACAGACTCAGAAAT 1657
Qy 521 AspProGluGlnGlyHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db 1658 AATCCAGGTATCAAAAGCATCTTAATTTGCTTTTCTGTTTCAAGTGAATTCATA 1717
Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyIleCysSer 560
Db 1718 AGCAACACATATTTCTTGAAGATTAAGCTCTCATATTAATCAAGAGATGCAATCTT 1777
Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuAsnAspSerPro 580
Db 1778 CCTGACATACAAACTCAGTGAAGAGAAACCAACATGCTTTGAAAAATGATTCACCC 1837
Qy 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1838 AGTAAACTATTTCCAGAACAGACCCCTGCTTCTGATGAATTTGCTCTGTTGGGATC 1897
Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrglyPheProGluAsnIleLeuGluSerHis 620
Db 1898 GTGAATGAGAGTTCATCTATTAATCTTATTTTCCACAAATATTTTGGAAAGCAC 1957
Qy 621 PheAsnArgIleSerLeuLeuGlyIle 629
Db 1958 TTCAATAGGATTTCACTTGGAAAAAG 1984

RESULT 12
US-09-972-708-22
Sequence 22, Application US/09972708
Publication No. US2003005987A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972, 708
CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 1698
TYPE: DNA
ORGANISM: Homo sapiens
US-09-972-708-22

Alignment Scores:
Pred. No.: 0 Length: 1698
Score: 2952.00 Matches: 562
Percent Similarity: 89.3% Conservative: 0
Best Local Similarity: 89.3% Mismatches: 3
Query Match: 88.8% Indels: 64
Gaps: 1

US-10-667-289-2 (1-629) x US-09-972-708-22 (1-1698)

Qy 1 MetAsn***ValThrIleGlnThrPheAlaValIleLeuTyrglyIleLeuPheSerTrp 20
Db 1 ATGAATCAGCTGCTATTTCAATGAGATGCAAGTATAGCCCTTTATCAATCTTCACTGG 60
Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleThrValGluProAlaThr 40
Db 61 TGTCAAGAGAAATTAACAATTAATTAATCTGCGCCACATCTGGGTAGAACAGCCACA 120
Qy 41 ILePheLeuMetGlyMetAsnIleSerIleTyrglyGlnAlaAlaIleLeuAsnGlyGln 60
Db 121 ATTTTAAAGTGGATTAATATCTATATATTTGCCAAGCAGACATTAAGAACTGGCAA 180
Qy 61 ProArgIleLeuHisPheTyrglyAsnGlyIleGlyGluArgPheGlnIleThrArgIle 80
Db 181 CCAAGGAACTTATTTTATAAAATGGCATCAAGAAAGATTTCAATCACAAGATT 240
Qy 81 AsnLeuThrThrAlaArgLeuTrpTyrglyAsnPheLeuGluProHisAlaSerMetTyrg 100
Db 241 AATTAACCAACACTGCGCTTGTGATTAATAAACTTCTGGAACACATGCTTCTATGTAC 300
Qy 101 CysThrAlaGluCysProIleHisPheGlnGluThrLeuIleCysGlyIleAspIleSer 120
Db 301 TGCATGCTGAAATGTCCTCAAACTTTTCAAGACACTGATATGTGAAAAAGCATTTCT 360
Qy 121 SerGlyTyrglyProProAspIleProAspGluValThrCysValIleTyrglyTyrgly 140
Db 361 TCTGATATCTGCGCAGATATTTCTGATGAAGTACCTGTCTATTAATATTCAGGC 420
Qy 141 AsnMetThrCysThrTrpAsnAla***IleLeuThrTyrglyIleAspThrIleVal 160
Db 421 AACATGCTTGACCTGGAATGCTGGAGACTCACTCAATACACAAATACGTGTGTA 480
Qy 161 HisValIleSerLeuGluThrGluGluGlnGlnIleTyrglyLeuThrSerSerTyrgly 180
Db 481 CATGTGAAGATTTAAGACAGAAAGAGCAACAGATCTCACTCAAGACTATATTAC 540
Qy 181 ILeSerThrAspSerLeuGlnGlyIleValTyrglyTyrglyValTrpValGlnAlaIleAsn 200
Db 541 ATCTCCACTATTCATTAACAAGGTGGCAAGAAATGTACTGTGTGGGCCAAGACGAAAC 600
Qy 201 AlaLeuGlyMetGluGluSerIleGlnIleGlnIleHisIleAsnAspAspIleValIlePro 220
Db 601 GCACTAGGCAATGAGAGTAAAGTAAACATGCAAAATTCACCTGATATTAATAGATACCT 660
Qy 221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProlySerThrIleIle 240
Db 661 TCTGCAAGCTGCTATTTCCAGAGCTGAGACATTAATCTCAAGTCCCAAGACCATTAAT 720
Qy 241 TyrglyAspSerGlnThrThrIleGluValIleSerCysGluMetArgTyrglyAlaThr 260
Db 721 TATTGGATAGTCAACCAATTTGAAAAAGTTTCTGTTGATAATGAGATCAAGGCTACA 780
Qy 261 ThrAsnGlnThrTrpAsnValIleGluPheAspThrAsnPheThrTyrglyGlnIleSer 280
Db 781 ACAACCAAACTTGAATGTTAAAGATTTGACCACAATTTTACATATGTGCAACAGTCA 840

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QY 281 GluPheTyrLeuGluProAsnIleValPheGlnValArgCysGlnGluThrGly 300
DB 841 GAATTCACCTGGAGCCAACTTAAGTACCTATTTCAGAGAGATGCAAGAAACAGGC 900
QY 301 LysArgTyrTrpGlnProTyrSerSerProPhePheHisValThrProGluThrValPro 320
DB 901 AAAAGGACTGGCAGCCTTGAGAGTTCACCTGTTTTCATATAAACACCTGAA----- 951
QY 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
DB 951 ----- 951
QY 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
DB 951 ----- 951
QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
DB 951 ----- 951
QY 381 ArgThrGlyIleLysValGlnGlyIleLeuLeuLeuIleProLysTrpLeuTyrGlyAspIle 400
DB 952 ---ACAGGAGATTAAAGAGAGATCTTAATGTTAATACCAAGTGGCTTTATGAAAGATATT 1008
QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420
DB 1009 CCTAATATGAAAAACACCAATGTTGTAATAATGCTACAGGAAATAGGAACTTATGAAAT 1068
QY 421 AsnAsnSerSerGlnGlnValLeuTyrValAspProMetIleThrGlnIleLysGlnIle 440
DB 1069 AATPATTTCCAGTGGAGAGCTCTTAATGTTGATCCCATGATTAACAGAGATTAAGAAATC 1128
QY 441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
DB 1129 TTCAATCCAGAACACCAAGCCTACAGCTACAGAGAGAAATACAGACCCCTGGAGACA 1188
QY 461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrValValTyrIleProAspLeu 480
DB 1189 AGAGACTACCGGCAAACTGCTATTCGACATATCTAGTATATATCTCTGATCTC 1248
QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluGlySerHisLeuSerAsn 500
DB 1249 AACGCTGGATTAACCCCAATTTTCAATTTTCTGCTGAGGAGAACCATTCAGCAAT 1308
QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
DB 1309 AATPATGAAATTACTCTTAACACTTAACACACAGTGTATCTTAGACTCAGAAAT 1368
QY 521 AsnProArgLeuGlnLysIleProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
DB 1369 AATCCCGAGTTTACAAAGCAATCTTAATTTGCTTTCTGTTCAAGTGAATTCATA 1428
QY 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyLysSerSer 560
DB 1429 AGCAACACATATTTCTTGGAGATTAAAGCTCTCATATTAATCAAGAGATGCAATCT 1488
QY 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
DB 1489 CCGTACATCAAAACCTCAGTAGAGAGAGAAACCACTGCTTTGGAAAAATGATTCAACC 1548
QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValLysCysGlnGlyIle 600
DB 1549 AGTGAAACTATTCAGAACAGACCTCTTCGATATAATTTGCTCTGTTGGGGATC 1608
QY 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
DB 1609 GTGATAGAGAGTGGCATCTATTAATACTTATTTTCCACAAATATTTTGGAAAGCAC 1668
QY 621 PheAsnArgIleSerLeuLeuGluLys 629
DB 1669 TTCAATAGGATTCACCTTGGAAAG 1695

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RESULT 13
US-10-715-667-22
; Sequence 22: Application US/10715667
; Publication No: US2004015216A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-715-667-22

Alignment Scores:
Pred. No.: 0          length: 1698
Score: 2952.00       Matches: 562
Percent Similarity: 89.3%    Conservative: 0
Best Local Similarity: 89.3%  Mismatches: 3
Query Match: 88.8%          Indels: 64
DB: 8                  Gaps: 1

US-10-667-289-2 (1-629) x US-10-715-667-22 (1-1698)
QY 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTyr 20
DB 1 ATGATCAGGTCACTATTCAATGAGATGAGATAGCCCTTACATACATCTTCAGCTGG 60
QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
DB 61 TGTCAAGGAGAAATTCAAATATTAATCTGCTGGCCCATCTGGGTAGAACCAACCA 120
QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
DB 121 ATTTTAAAGTGGTATGAAATATCTCTATATATTCACAGCAGCAATTAAGACTGCCAA 180
QY 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
DB 181 CCAAGGAACTTCATTTTATAAATAATGCATCAAGAAAGATTTCAATCACAAGGATT 240
QY 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
DB 241 AATTAACACACACAGCTGGCTTGTGTATTAATACTTTCTGGAACACATGCTTATGTAC 300
QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
DB 301 TGCATCGCGAAAGTCCCAACATTTTCAAGAACACTGATATGAGAAAGACATTTCT 360
QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
DB 361 TCTGGATATCCGCAGATATTTCTGATGAAGTAACTGCTGATTAATGAATATTCAGGC 420
QY 141 AsnMetThrCysThrTrpAsnAla**LysLeuThrTyrIleAspThrLysTyrValVal 160
DB 421 AACATGACTTGACCTGGAGATGCTGGAGAGCTCACCTACATACACAAATATCGTGTA 480
QY 161 HisValLysSerLeuGluThrGluGluGlnGluGlnGluTyrLeuThrSerSerTyrIleAsn 180
DB 481 CATGTAAAGATTTAAGACAGAAAGAACCAAGTATTTCACTCAGCTATATTAAC 540
QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTrpValGlnAlaIleAsn 200

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Db 541 ATCTCAGTATTCATTACAAAGTGGCAAGAAAGTACTGGTGGTCCAGCAAGCAAC 600
 Qy 201 AlaleuGlyMetGluGluSerGlyGluLeuGlnIleHisLeuAspAspIleValIlePro 220
 Db 601 GCACCTAGGCATGGAAGAGTCAAAACCTGCAATTCACCTGGATGATATAGTATTCCT 660
 Qy 221 SerAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
 Db 661 TCTGCACCCGCTCATTTCCAGGGCTGAGACTATAAATCTACAGGCCCAAGACCATATTT 720
 Qy 241 TyrThrAspSerGlnThrThrIleGluLysValSerGlyMetAspGlyLysValIleThr 260
 Db 721 TATTGGATAGTCAAAACCAATGAAAGGTTTCCGTGAAAGAAAGATTCAGAGCTCA 780
 Qy 261 ThrAsnGlnThrTrpAsnValIleGluPheAspThrAsnPheThrValAlaGlnIleSer 280
 Db 781 ACAACCCAACTGGAAATGTTAAGAAATTTGACCCAAATTTTACATATGTCACACATCA 840
 Qy 281 GluPheGlyLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
 Db 841 GAATTTACTTGGAGCCAAACATTAAGTACGTATTTCAAGTGAATGTCAGAAACAGGC 900
 Qy 301 LysArgGlyTrpGlnProLysSerSerProPhePheHisLysThrProGluThrValPro 320
 Db 901 AAAAGGTACTGGCAGCCCTGGAGTTCACTGTTTTTCATATAAACACCTGAA----- 951
 Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
 Db 951 ----- 951
 Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
 Db 951 ----- 951
 Qy 361 IleValPheAlaValMetLeuSerIleLeuSerIleGlyIlePheAsnArgSerPhe 380
 Db 951 ----- 951
 Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuGlyAspIle 400
 Db 952 ----ACAGGATTAAGAAAGATCTTATTTGTTATACCAAGTGGCTTTATGAAGATATT 1008
 Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnIleAsnSerGluLeuMetAsn 420
 Db 1009 CCTATATGAAACACAGCAATGTTGTGAAATGCTACAGAAATAGTGAATCTTATGAAT 1068
 Qy 421 AsnAsnSerSerGluGlnValLeuTyrValAspProMetIleThrGluIleLysGluIle 440
 Db 1069 AATATATTCAGTGGAGAGTCTCTATATGTTGATCCCATGATTTACAGAGATTAAGAAATC 1128
 Qy 441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
 Db 1129 TTTCATCCAGAACACAAAGCTACAGACTACAGAAAGAAATACAGAACCCCTGGAAACA 1188
 Qy 461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrValValTyrIleProAspLeu 480
 Db 1189 AGAGACTACCCGAAACTCGCTATTCGACATACATCAAGTGTATATATCTCGATCTC 1248
 Qy 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluLysSerHisLeuSerAsn 500
 Db 1249 AACCTGGATATAAACCCCAATTTTCAATTTTGTGCTGAGGAGAGCCATCTAGCAAT 1308
 Qy 501 AsnAsnGluIleThrSerLeuThrLeuLysProValIleAspSerLeuAspSerGlyAsn 520
 Db 1309 AATATATGAATTAATCTTCTTAACACTTAACCAACCAAGTGTATCTTAAGACTCAGGAAT 1368
 Qy 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
 Db 1369 AATCCCAAGTATCAAAAGCATCTTAATTTCTTTCTGTTTCAAGTGAATTCACATA 1428
 Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyLysCysSerSer 560
 Db 1429 AGCAACACAAATATTTCTTGAGAAATTAGCCTCATATTAATCAAGAGAAATGCAATTC 1488

Qy 561 ProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
 Db 1489 CCGACATACAAAAACCTCAGTAGAGAGAGAAACCAACCATGCTTTTGGAAAAATGATTCACCC 1548
 Qy 581 SerGluThrIleProGluGluThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
 Db 1549 AGTGAACATATTCCAAAACAGACCCTGCTTCGATGAATTTGTCCTGTTTGGGGATC 1608
 Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
 Db 1609 GTGAATGAGAGTGGCATTTATTAATCTTAATTTTCCACAAATATTTTGGAAAGCCAC 1668
 Qy 621 PheAsnArgIleSerLeuLeuGlyLys 629
 Db 1669 TTCAATAGATTTTCACTTGGAAAAAG 1695
 RESULT 14
 US-09-972-708-29
 / Sequence 29, Application US/09972708
 / Publication No. US2003059871A1
 / GENERAL INFORMATION:
 / APPLICANT: Immunex Corporation
 / APPLICANT: Cosman, David J.
 / APPLICANT: Mosley, Bruce A.
 / APPLICANT: Bird, Timothy A.
 / APPLICANT: Dubose, Robert F.
 / APPLICANT: Wiley, Steven R.
 / TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
 / FILE REFERENCE: 3160-B
 / CURRENT APPLICATION NUMBER: US/09/972,708
 / CURRENT FILING DATE: 2001-10-05
 / NUMBER OF SEQ ID NOS: 29
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 29
 / LENGTH: 1935
 / TYPE: DNA
 / ORGANISM: Mus musculus
 / US-09-972-708-29
 Alignment Scores:
 Pred. No.: 5,93e-244 Length: 1935
 Score: 2280.50 Matches: 432
 Percent Similarity: 78.2% Conservative: 76
 Best Local Similarity: 66.5% Mismatches: 115
 Query Match: 68.6% Indels: 27
 DB: 3 Gaps: 4
 US-10-667-289-2 (1-629) x US-09-972-708-29 (1-1935)
 Qy 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrp 20
 Db 1 ATAGAGTCACTCAACACTTCAGCTGCAATGTGTATAGCCCTTTATATGCTTCAAGATG 60
 Qy 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThr 40
 Db 61 TGTCAAGAGAAATCAACAATATTAATCTGCTGTGGTCACTGTGGGTGAGCTGTGTGAA 120
 Qy 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCysGln 60
 Db 121 ATTTTCAGATGGGCAATAATGTTCTATATATTTGCCAAGAGCCCTTAAGCACTGCCA 180
 Qy 61 ProArgLysLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
 Db 181 CCAAGGAATCTTACTTTATTAATAATGCTTCAAGAAAGAAATTTGATATCAAGAGATT 240
 Qy 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
 Db 241 AATGAACAACAACACTCGAATTTGTATTAAGGCTTTTCGGAACCTCATATGATCAT 300
 Qy 101 CysThrIleGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
 Db 301 TGCACTGTGAATGTCTGTGCTATTTTCAAGACACTGATTTGTGGAAAAAGCAATTC 360


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Db      1 ATGAGTCACTGACACTTCAGTCGATGTGTGATGATGACCCCTTATATGCTCTTCAGATGG 60
Qy      21 CysHisGlyGlyIleThrAsnIleAsnGlySerGlyHisIleThrValGluProIleThr 40
Db      61 TGTCAAGGAGGAAATCACAAGATATACTGCTCTGTGTACATGTGGTGGACCTGGGAA 120
Qy      41 IlePheLeuMetGlyMetAsnIleSerIleThrCysGlnAlaAlaIleValAsnGlyGln 60
Db      121 ATTTTCAGATGGGCAATTAATGTTTCTATATATGTCAGAAAGGCCCTTAAGCACTGCCGA 180
Qy      61 ProArgIleLeuHisPheThrIleValAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80
Db      181 CCAAGGAATCTTATCTTTATATAAAATGCTTCAAAAGAAATTTGATATACAAAGAAAT 240
Qy      81 AsnIleThrThrAlaArgLeuThrPheThrIleValAsnPheLeuGluProHisAlaSerMetThr 100
Db      241 AATGGAACAACAGCTCGGATTTGGTATTAAGCCTTTTCGAAAGCTCAAGCTCATATGAT 300
Qy      101 CysThrAlaGluCysProLeuHisPheGlnGluThrLeuIleCysGlyIleValAspIleSer 120
Db      301 TGCACCTGCAATGCTCGGTCAATTTCAAGAGACATGATTTGTGGGAAAGACATTTCC 360
Qy      121 SerGlyThrProProAspIleProAspGluValThrCysValIleThrGlyIleThrSerGly 140
Db      361 TCTGACATCCACCGAGTCCCGCCAGCAATCTGACATGTGATGATTAATGATCTCAGGC 420
Qy      141 AsnMetThrCysThrTPAsnAla**LysLeuThrThrIleAspThrIleValVal 160
Db      421 AACATGACATGCACTGGAACACCTGGGAACCTTACATACATGATACCAAGTATATG 480
Qy      161 HisValIleSerLeuGluThrGluGluGluGluGluGluGluGluGluGluGluGluGlu 180
Db      481 CATGTGAAGAGTTGGAGACAGAAAGAAACAACAATATCTGCTCAAGCTAATGTTAAG 540
Qy      181 IleSerThrAspSerLeuGluGlyIleValIleValIleValIleValIleValIleVal 200
Db      541 ATCTCCACTGACTCTACAGGACAGAGCAAGATTTGTATGTATGTATGTATGTATGTAT 600
Qy      201 AlaLeuGlyMetGluGluSerLeuGluGluGluGluGluGluGluGluGluGluGluGlu 220
Db      601 TCCCTAGGCACTGGAACCTCAACAACATCTACATCTGATGATATATGATATCT 660
Qy      221 SerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
Db      661 TCTGCGTCATCATTTCCAGGCTGAGACATAACAACATCTGATCAACCAAGACATAGTT 720
Qy      241 TyrThrAspSerGlnThrIleGluIleValIleSerGlyMetArgGlyIleValIleThr 260
Db      721 TACTGGAAGAAAGCAAACTATGATGAGAAAGATTTCTGTAGATGATGATCAAAAACA 780
Qy      261 ThrAsnGlnThrTPAsnValIleGluIlePheAspThrAsnPheThrIleValIleGlnIleSer 280
Db      781 ACAACCAAAAGCTGAGATGTTAAAGATTTGAAGCCCAATTTCAATATGATACAGCATCA 840
Qy      281 GluPheThrLeuGluProAsnIleLysThrValIlePheGlnValArgCys----- 296
Db      841 GAATTTACTCTGAGCAGACAGCAAGATATGATTTCAAGTGCATGTCAAGAAACTGCT 900
Qy      297 -----GlnIleThrGly 300
Db      901 AAAAGAACTGGCAGCCTGGAGTTCCCTTTGTCCACCAAACTTCCCAAGAAAGCTGT 960
Qy      301 LysArgThrIleProIleProIleProIleProIleProIleProIleProIleProIlePro 320
Db      961 AAAAGAAAGCTGGCAGCCTGGAGTTCCCTTTGTCCACCAAACTTCCCAAGAAAGCTGT 1020
Qy      321 GlnValIleSerIleValIlePheGlnIleAspThrIleProAsnGlyIleValIleSer 340
Db      1021 CAGGTTACAGCAAAATCA---TCCACCAAGCTCAGAAAGATGAGATGCTCAGGCTACA 1077
Qy      341 IleSerThrGlyIleLeuThrSerAspAsnArgIleValIleGlyLeuLeuLeuGlyMet 360
Db      1078 ATCTTCAGAGACATCTGCTTCAAGTATCATCAAGACATTTGTTGTGGGAATG 1137

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Qy      361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db      1138 GTCTTCTGGCCATCATGTTGGCCGATTTTCTCTGATTTGGATATTAACAATCAATCACTT 1197
Qy      381 ArgThrGlyIleLysArgAlaGluIleLeuLeuIleProLysThrPheLeuThrGluAspIle 400
Db      1198 CGATAGGAATTAAGAAAGAAAGTTTATCTGATATATCCAAAGTGGCTTTATGAAAGATATT 1257
Qy      401 ProAsnMetLysAsnSerAsnValIleLysMetLeuGlnIleAsnSerGluLeuMetAsn 420
Db      1258 CTTAATTTGGAATAATGCAATGTTGCAAAATTTATACAGAAATAAAGTATTTGAGAAAT 1317
Qy      421 AsnAsnSerSerGluGluValIleThrValIleAspProMetIleThrGluIleGlyIle 440
Db      1318 GATATAGCCAGTACAGCAGGCCCTGTATGTGATCTGTCTTACAGAGATTAAGTAAATC 1377
Qy      441 PheIleProGluHisIleLysProThrAspThrIleLysGluAsn---ThrGlyProLeuGlu 459
Db      1378 TCTCCCTGGAAACAAACCCACAGATTACAAAGAAAGAGCTCACAGACCTCTTGAG 1437
Qy      460 ThrArgAspThrProGluAsnSerLeuPheAspAsnThrThrValIleThrIleProAsp 479
Db      1438 ACAAGACATGCTCTTGAAGATGTTGTCTACCACTTCTGTGTGTATATCTTGAC 1497
Qy      480 LeuAsnThrGlyThrLysProGluIleSerAsnPheLeuProGluGlySerHisLeuSer 499
Db      1498 CTCACACCTGATATCAAAACCCAGGTTTCAAAATGTTCTCTCGAGAGAAACCTTTCAAT 1557
Qy      500 AsnAsnAsnGluIleThrSerLeuThrLeuLysProProValIleAspSerLeuAspSerGly 519
Db      1558 AACAGAGATGAAGAGACCTACATCCCTTGAACCAACAGATACCACTT----- 1608
Qy      520 AsnAsnProArgLeuGluLysHisProAsnPheAlaPheSerValIleSerValIleSer 539
Db      1609 -----GCCAGTTGAAACATATCCCACTTCAATTTCTCTCAAGATATGCTTTA 1662
Qy      540 LeuSerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGluGlyCysSer 559
Db      1663 CTAACAAACACATATCTTGATGATATGTCCTGTTTAATCAAGAGAAATTCAT 1722
Qy      560 SerProAspIleGluAsnSerValIleGluGluIleThrIleMetLeuLeuGluAsnAspSer 579
Db      1723 TCTCTTGACATTAATAAACTCAAGACAGAGAAACCAAGCATCGTTTGCAAAAGTACTCA 1782
Qy      580 ProSerGluThrIleProGluGluIleThrLeuLeuProAspGluPheValIleSerCysLeuGly 599
Db      1783 CCCAGTGAACATATCCAGGCGAGACTCTGTGTCTGATGAAATTTGTCTCTGTTGGCA 1842
Qy      600 IleValAsnGluLeuProSerIleAsnThrIlePheProGluAsnIleLeuGluSer 619
Db      1843 ATGGGATGAGACATTCATATTAATCTTCACTTCCACAGAACGTTTGGAAAGC 1902
Qy      620 HisPheAsnArgIleSerLeuLeuGluLys 639
Db      1903 CATTTCAGTGAATTTCACTTCCAAAG 1932

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Search completed: October 14, 2006, 17:25:45
 Job time : 2007 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: October 14, 2006, 14:43:19 / Search time 365 Seconds
(without alignments)
4829.870 Million cell updates/sec

Title: US-10-667-289-2

Sequence: 1 MNXYTIQMDVIALYILFSW.....TYPQNIISHFNRISLEK 629

Scoring table:

BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published.Applications.NA.New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs602h
-USBR=US10667289 -OCGN_1_1_238 -runat_13102006_111543_24573 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLIST -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:*
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9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	3314	99.6	1910	8 US-11-274-375-9
2	3292	99.0	2123	8 US-11-274-375-5
3	2192	65.9	1301	8 US-11-274-375-7
4	2175	65.4	1479	8 US-11-274-375-3
5	1695	51.0	1784	8 US-11-274-375-1
6	286	8.6	360	8 US-11-274-375-23
7	216	6.5	4040	8 US-11-266-748A-32008

8	209	6.3	3085	8 US-11-266-748A-28955	Sequence 28955, A
9	203	6.1	3159	8 US-11-266-748A-31490	Sequence 31490, A
10	190	5.7	2723	8 US-11-330-726-179	Sequence 179, App
11	190	5.7	2736	6 US-10-669-920-109	Sequence 109, App
12	190	5.7	3162	8 US-11-266-748A-29132	Sequence 29132, A
13	189	5.7	1869	7 US-11-330-726-180	Sequence 180, App
14	188	5.7	5252	6 US-10-511-937-3101	Sequence 3101, App
15	188	5.7	5252	6 US-10-511-937-3102	Sequence 3102, App
16	186.5	5.6	1989	7 US-11-353-451-7	Sequence 7, Appli
17	186.5	5.6	2199	7 US-11-353-451-5	Sequence 5, Appli
18	186.5	5.6	2903	9 US-11-301-764-4	Sequence 4, Appli
19	173	5.2	2295	9 US-11-301-764-38	Sequence 38, Appli
20	170	5.1	1557	7 US-11-353-427-5	Sequence 5, Appli
21	170	5.1	1557	9 US-11-353-454-5	Sequence 5, Appli
22	170	5.1	1557	9 US-11-301-764-70	Sequence 70, Appli
23	165.5	5.0	1716	8 US-11-300-928-28	Sequence 28, Appli
24	165.5	5.0	1790	8 US-11-286-092-31	Sequence 31, Appli
25	165.5	5.0	1790	8 US-11-286-155-31	Sequence 31, Appli
26	165	5.0	1425	6 US-10-669-920-101	Sequence 101, App
27	163.5	4.9	2583	8 US-11-266-748A-56095	Sequence 56095, A
28	163.5	4.9	3003	6 US-10-511-937-2820	Sequence 2820, Ap
29	163.5	4.9	3029	8 US-11-266-748A-27795	Sequence 27795, A
30	160.5	4.8	1344	6 US-10-669-920-107	Sequence 107, App
31	157.5	4.7	1989	7 US-11-353-451-13	Sequence 13, Appli
32	157.5	4.7	2728	9 US-11-301-764-113	Sequence 113, Appli
33	157.5	4.7	2748	7 US-11-353-427-7	Sequence 7, Appli
34	157.5	4.7	2748	7 US-11-353-454-7	Sequence 7, Appli
35	157.5	4.7	2748	9 US-11-301-764-111	Sequence 11, App
36	155.5	4.7	2356	6 US-10-669-920-94	Sequence 94, Appli
37	153	4.6	975	7 US-11-353-451-9	Sequence 9, Appli
38	148	4.4	1827	7 US-11-330-726-177	Sequence 177, App
39	148	4.4	1831	7 US-11-330-726-176	Sequence 176, App
40	147	4.4	720	7 US-11-353-451-11	Sequence 11, Appli
41	140.5	4.2	4968	8 US-11-266-748A-31664	Sequence 31664, A
42	140.5	4.2	5157	8 US-11-266-748A-56701	Sequence 56701, A
43	139.5	4.2	1538	8 US-11-266-748A-250506	Sequence 250506, A
44	139.5	4.2	1538	8 US-11-266-748A-311023	Sequence 311023, A
45	139	4.2	1101	6 US-10-669-920-103	Sequence 103, Appli

ALIGNMENTS

RESULT 1
US-11-274-375-9
Sequence 9, Application US/11274375
Publication No. US20060106201A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masaatsu
TITLE OR INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
FILE REFERENCE: 06501-105U81
CURRENT APPLICATION NUMBER: US/11/274, 375
CURRENT FILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: US/10/105, 930
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/JP00/06654
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: JP 2000-240397
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP 11-273358
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1910
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1887)
US-11-274-375-9

Alignment Scores:

Pred. No.: 3,74e-315 Length: 1910
 Score: 3314.00 Matches: 626
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 3
 Query Match: 99.6% Indels: 0
 DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-9 (1-1910)

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 QY 21 CysHisGlyGlyIleThrAsnIleAsnCysSerGlyHisIleTyrValGluProAlaThr 40
 Db 61 TGTCAATGAGGAATTAACAATATATACCTGCTGGCCACATCTGGTGAACAACGCCACA 120
 QY 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleValSerCysGln 60
 Db 121 ATTTTAAAGATGGGTAAATATCTATATATATGCAAGCAAGCAATTAAGAACTGCCAA 180
 QY 61 ProArgLeuHisPheTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
 Db 181 CCAAGGAACTTCCTTTTATTAATAATGGCATCAAGAAAGATTCAAAATCACAGGAATT 240
 QY 81 AsnLysThrThrAlaArgLeuTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
 Db 241 AATTAACAACAGCTCGGCTTGGTATTAATACTTCGGAACCAATGCTTATGTAC 300
 QY 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
 Db 301 TGCACTCGTGAATGCCAAACATTTTCAAGAGACCTGATATGTGAAGAAAGACATTTCT 360
 QY 121 SerGlyTyrProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
 Db 361 TCTGGATATCCGCCAGATATCTCGATGAAGTAACTGTGCATTTATGAATATTCAGGC 420
 QY 141 AsnMetThrCysThrTPRAsnAla**LysLeuThrTyrIleAspThrLysTyrValVal 160
 Db 421 AACATGACTTGCACTGGAATGCTGGAAAGCTCACATACATAGACAAATAATGTGTA 480
 QY 161 HisValLysSerLeuGluThrGluGluGluGlnIleThrLeuThrSerSerTyrIleAsn 180
 Db 481 CATGTGAAGAGTTTGAAGACGAAGAAAGACACAGATCTCACTCAAGGTATATTAAC 540
 QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTPRValGlnAlaAsn 200
 Db 541 ATCTCCACTGATTCATTAACAAGGTGGCAAGAAAGTACTTGGTTGGTCCAAAGCAGCAAC 600
 QY 201 AlaLeuGlyMetGluLysSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
 Db 601 GCACTAAGGATGGAAGATCAAAACAACCTGCAAAATTCACCTGATGATATGATACCT 660
 QY 221 SerIleAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLysThrIleIle 240
 Db 661 TCTGCAACCGCATTTCCAGGGCTGAGACATTAATATGCTACAGGCCCAACACATTAATT 720
 QY 241 TyrTPRAspSerGlnThrThrIleGluLysValSerCysGluMetCysArgTyrLysAlaThr 260
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 QY 261 ThrAsnGlnThrTPRAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
 Db 781 ACAAAACCAACTTGAATGTTAAAGAATTGACACCAATTTTACATATGTGCAACAGTCA 840
 QY 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValaGlySerGlnGluThrGly 300
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 QY 301 LysArgTyrTPRGLuProTyrSerSerProPhePheHisLysThrProGluThrValPro 320
 Db 901 AAAAGGACTGGAGCCTTGGAGTTCACTGTTTTCATTAATAACCTGAAACAGTTCCC 960

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 QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
 Db 1081 ATCGTCTTGTGTATGTTGTCATATCTTCTTTGATGGATATTAACAATCATTC 1140
 QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrPheLysTyrGluAspIle 400
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 QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeuMetAsn 420
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 QY 441 PheIleProGluHisLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
 Db 1321 TTCACTCCAGAACACAAAGCTTACAGACTTCAAGAAAGAAATACAGAGCCCTGGAGACA 1380
 QY 461 ArgAspTyrProGlnAsnSerLeuPheAspAsnThrThrValValTyrIleProAspLeu 480
 Db 1381 AGAGACTACCCGAAACCTGCTATTCGACAAATACATACAGTTGATATATCTGATCTC 1440
 QY 481 AsnThrGlyTyrLysProGlnIleSerAsnPheLeuProGluLysSerHisLeuSerAsn 500
 Db 1441 AACATGATATTAACCCCAATTTTCAATTTTCTGCTGAGGAAAGCCATCTCAGTAAT 1500
 QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
 Db 1501 AATPATTAATTAATCTTCTTAAACATTAACCAACAGTTGATATCTTGAACCTGAGAAAT 1560
 QY 521 AsnProArgLeuGlnLysHisProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
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 QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
 Db 1741 AGTGAACATATTCAGAACAGACCCCTGCTCTGATGAATTTGTCTCTTGTGGGATC 1800
 QY 601 ValAsnGluLysProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
 Db 1801 GTGAATGAGAGTTGGCATATTAATTAATCTTATTTTCAAAAATATTTTGAAGAACAC 1860
 QY 621 PheAsnArgIleSerLeuLeuGlyLys 629
 Db 1861 TTCAATGAGATTCACCTTGGAAAG 1887

RESULT 2

US-11-274-375-5

; Sequence 5, Application US/11274375

; Publication No. US20060106201A1

; GENERAL INFORMATION:

; APPLICANT: Maeda, Masatsugu

; APPLICANT: Yasuchi, Noriko

; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12

; FILE REFERENCE: 06501-105051

CURRENT APPLICATION NUMBER: US/11/274,375
CURRENT FILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: US/10/105,930
PRIOR FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/JP00/06654
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: JP 2000-240397
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP 11-273358
PRIOR FILING DATE: 1999-09-27
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SEQ ID NO 5
LENGTH: 2123
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (98)...(1984)
US-11-274-375-5

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Score: 3292.00 Matches: 622
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Best Local Similarity: 98.9% Mismatches: 5
Query Match: 99.0% Indels: 0
DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-5 (1-2123)

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Db 158 TGTGATGAGGAATTAACAATATTAACCTGCTGCGCAACATCTGGTGAACAGCCACA 217

Qy 41 IlePheLeuMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleValAsnCysGln 60
Db 218 ATTTTAAAGTGGGTGGAATATCTCTATATATTGCCAAGCAGCAATTAAGAACTGCGCAA 277

Qy 61 ProArgLeuHisPheTyrIleValAsnGlyIleLeuGluArgPheGlnIleThrArgIle 80
Db 278 CCAAGGAACTTCACTTTTAAATAATGCGATCAAGAAAGATTCAAATCAAGAAGATT 337

Qy 81 AsnLeuThrAlaAlaGluLeuTyrIleValAsnPheLeuGluProHisAlaSerMetTyr 100
Db 338 AATTAACAACAGCTCGCTTGGTATTAATAAATCTTCTGGAACACATGCTTCTATGTAC 397

Qy 101 CysThrAlaGluCysProLeuHisPheGlnGluThrLeuIleCysGlyValAspIleSer 120
Db 398 TGCACGCTCAATGTCCCAACATTTTCAAGAGACACTGATGTGAAAAAGACATTTCT 457

Qy 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
Db 458 TCTGGATATCCGCGCAATTTCTGATGAAGTAACCTGTGCTTATTAATATTCAGGC 517

Qy 141 AsnMetThrCysThrTyrAsnAla**LysLeuThrTyrIleAspThrIleValVal 160
Db 518 AACATGACTTGCACCTGGAAATGCTGGAGGCTCACATACATAGACAAATAATAGTGTA 577

Qy 161 HisValIleSerLeuGluThrGluGluGluGluGluGluGluGluGluGluGluGluGlu 180
Db 578 CATGTGAAGAGTTTGAAGACAGAAAGAGACAGACAGATCTCACTCAAGGTATATTAAC 637

Qy 181 IleSerThrAspSerLeuGluGlyIleValSerTyrIleValIleValIleValIleVal 200
Db 638 ATCTCCCTGATTCATTAACAGGTGCGAAGAGTACTTGGTTGGGTCCAGCGCAAC 697

Qy 201 AlaLeuGlyMetGluSerIleValIleGluGluIleHisIleAspAspIleValIlePro 220

Db 698 GCACTAGGATGAGAGATGCAAAACATGCAAAATTCACCTGATGATATAGTACTT 757
Qy 221 SerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrValProLeuThrIleIle 240
Db 758 TGTGACCCGCTCATTTTCCAGGGCTGAGACTATTAATCTTACAGTCCCAAGACATTAAT 817

Qy 241 TyrTrpAspSerGlnThrThrIleGluValSerCysGluMetArgTyrValAlaThr 260
Db 818 TATTTGGATAGTCAACCAACATTTGAAGAGTTTCTGTGAATATGATATCAAGCTTACA 877

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Db 878 ACAACCAAACTTGATGTTAAAGATTGACACCAATTTTATCATATGTGCAACACTGCA 937

Qy 281 GluPheTyrLeuGluProAsnIleValTyrValPheGlnValArgCysGlnGluThrGly 300
Db 938 GAATCTACTTGGAGCCAAACATTAAGTATGATTTCAAGTGAATGTCAGAAACAGGC 997

Qy 301 LysArgTyrTrpGluProTyrPheSerProPhePheHisIleTyrThrProGluThrValPro 320
Db 998 AAAAGTACTGGCAGCTTGGAGTTCCTGTTTTTCAATAAACACCTGAACAGTTCC 1057

Qy 321 GluValThrSerIleValPheGlnHisAspThrTrpAsnSerGlyLeuThrValIleSer 340
Db 1058 CAGGTCAATCAAAAGCATTCCAACATGACATGAAATTCGGGCTAACAGTTGCTTCC 1117

Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyIleLeuLeuGlyMet 360
Db 1118 ATCTTACAGGGACCTTACTTCTGACACAGAGACATTTGACTTTTATTTGGAAATG 1177

Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1178 ATGCTCTTCTGTTATGTTGTCAATCTTCTTGAATGGACATTTACAGATCAATTC 1237

Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrLeuTyrGlyAspIle 400
Db 1238 CGAAGTGGATTAAGAAAGATCTTATGTATATACAAAGTGGCTTTATGAAGATATT 1297

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Db 1298 CTTAATATGAAACACGAATGTGTGAATAATGCTACAGAAATATGAACTTATATAT 1357

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Db 1358 AATTAATCCAGTGAAGAGGCTCTATATGTTGATCCCATGATTCAGAGATTAAGAAATC 1417

Qy 441 PheIleProGluHisLysProThrAspTyrLysLeuGluAsnThrGlyProLeuGluThr 460
Db 1418 TTCATCCAGAAACAAAGCTTACAGACTACAAAGAGGAATACAGGACCCCTGGAGACA 1477

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Db 1478 AGAGACTACCCGCAAACTGCTATTCGACAAATACACATTTGATATATTCCTGAATCTC 1537

Qy 481 AsnThrGlyTyrLysProGluIleSerAsnPheLeuProGluIleSerHisLeuSerAsn 500
Db 1538 AACATCGATATTAACCCCAATTTCAATTTCTGCTAGGAGAACCTTCATCAATAT 1597

Qy 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db 1598 AATTAATGAATTAATCTTCACTTAACATTAACCAACAGTTGATCTTAGACTCAGGAAT 1657

Qy 521 AsnProArgLeuGlnHisIleProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db 1658 AATCCAGGTTACAAAGACATCTTAATTTGCTTTTCTGTTTCAGATGGAATTCATA 1717

Qy 541 SerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyCysSerSer 560
Db 1718 AGCAACACATATTTCTTGGAGAAATTAAGCTCATATTAATCAAGAGAAATCAAGTTCT 1777

Qy 561 ProAspIleGlnAsnSerValIleGluGluThrThrMetLeuLeuGluAsnAspSerPro 580
Db 1778 CTTGACATACAAAACTCAGTAGAGAGAGAAACCAATGCTTTTGGAAATGATTCACCC 1837

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Qy 581 SerGluThrIleProGluGlnThrLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1838 AGTAAACATTCACGAACAGACCCCTCTCCGATGAAATTTGCTCTCTGTTGGGATC 1897
Qy 601 ValAsnGluGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHis 620
Db 1898 GTGATAGAGAGTTGCCATCATTAATACTAATTTCCACAAATATTTGGAAAGCCAC 1957
Qy 621 PheAsnArgIleSerLeuLeuGluLys 629
Db 1958 TTCAATAGAAATTCACCTTGAAAAAG 1984

RESULT 3
US-11-274-375-7
; Sequence 7, Application US/11274375
; Publication No. US20060106201A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, Noriko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/11/274,375
; PRIOR FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1284)
; US-11-274-375-7

Alignment Scores:
Pred. No.: 3e-205 Length: 1301
Score: 2192.00 Matches: 410
Percent Similarity: 99.3% Conservative: 0
Best Local Similarity: 99.3% Mismatches: 3
Query Match: 65.9% Indels: 0
DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-7 (1-1301)
Qy 1 MetAsn***ValThrIleGlnThrPaspAlaValIleAlaLeuTyrIleLeuPheSerTyr 20
Db 1 ATGATATCAGGTCACCTATTCATATGGAATGAGATGAGTAAATAGCCCTTTTCAATACCTCTTCAGCTGG 60
Qy 21 CysHisGlyGlyIleThrAsnIleAsnGlySerGlyHisIleTyrValGluProAlaThr 40
Db 61 TGTATGAGAGAAATTTACAAATATAACTGCTGCGCCACATCTGGATGAAACGACCA 120
Qy 41 IlePheIleMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnGlyGln 60
Db 121 ATTTTAAAGATGGGTATAGAAATATCTCTATATATGGCCAGAGCAATTAAGAACTGGCAA 180
Qy 61 ProArgIleLeuHisPheTyrTyrAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
Db 181 CCAAGAAACTTCATTTTATATAAAATGCGCATCAAGAAAGATTTCAATCAAGGATTT 240
Qy 81 AsnLysThrThrAlaArgLeuTyrTyrLysAsnPheLeuGluProHisAlaSerMetTyr 100
Db 241 AATAAAACAACAGCTCGCTTGATTAATAAAATTTCTGGAACACAGCTTCTATGTAC 300
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Qy 101 CysThrAlaGluCysProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSer 120
Db 301 TGCATGCTGTAATGTCCTCAAAACATTTTCAAGAGACCTGATATGTGAAAAAGCATTTCT 360
Qy 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGlyTyrSerGly 140
Db 361 TCTGATATCCGCAATATTCCTGATGAAAGTAACCTGTCTATTATGAAATATTCAGGC 420
Qy 141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTyrIleAspThrLysTyrValIle 160
Db 421 AACATGACTTGACACCTGGAATGCTGGGAAGCTCACCTACATACACAAATACGTGGTA 480
Qy 161 HisValIleSerLeuGluThrGluGluGlnGlnTyrLeuThrSerSerTyrIleAsn 180
Db 481 CATGTGAAGAGTTTAGAGACAGAAAGAACAGATATCTCACCTCAACCTATATTAAC 540
Qy 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTrpValGlnAlaAlaAsn 200
Db 541 ATCTCCAGATTCATTAACAGAGTGGCAAGAGTACTGTGTGGGTCCAGACGCAAC 600
Qy 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIlePro 220
Db 601 GCATAGGCAATGGAAGATGTAACAAACAGTCAAAATTCACCTGATATAGTATGATCCT 660
Qy 221 SerAlaAlaValIleSerArgIleGluThrIleAsnAlaThrValProLysThrIleIle 240
Db 661 TCTGCAAGCCGTATTCAGAGGCTGAGACTATAAATGCTCAGTGGCCCAAGACCATATTT 720
Qy 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetArgTyrLysAlaThr 260
Db 721 TATTTGATATGTAACAAACAAATGAAAGGTTCCGTGTAATATGAAATCAAGGCTACA 780
Qy 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGlnSer 280
Db 781 ACAACCAACCTTGAAATGTTAAAGAAATTTGACACCAATTTTCAATATGCAACAGTCA 840
Qy 281 GluPheTyrLeuGluProAsnIleLysTyrValPheGlnValArgCysGlnGluThrGly 300
Db 841 GAATTCATCTGAGGCCAAACATTAAGTACGATTTTCAAGTGAAGATGTCAGAAACAGGC 900
Qy 301 LysArgTyrTrpGlnProTyrPserSerProPhePheHisLysThrProGluThrValPro 320
Db 901 AAAAGGACTGGGACCTTGAGGTCACTGTTTTCATTAACACCTGAAACAGTTCCC 960
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThrTrpAsnSerGlyLeuThrValAlaSer 340
Db 961 CAGGTACATCAAAAGATTCCAACATGACATGGAATTCGGGGTAAACAGTTGGCTTC 1020
Qy 341 IleSerThrGlyHisLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMet 360
Db 1021 ATCTCTACAGGGACCTTACTCTGACACAGAGGAGACATTTGAGACTTTTATTTGGGATG 1080
Qy 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1081 ATGCTCTTCTGTTATGTTGATGTCATTCCTTTGATTTGGATATTTTAAACATCATTC 1140
Qy 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysThrPheLysTyrGluAspIle 400
Db 1141 CGAAGCTGGATTTAAAGAAAGATCTTATTTGTTATATCCAAAGTGGCTTTATGAAGATTT 1200
Qy 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGln 413
Db 1201 CTTAATATGAAAAACAGCAATGTTGTGAAATATGCTACAG 1239

RESULT 4
US-11-274-375-3
; Sequence 3, Application US/11274375
; Publication No. US20060106201A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, Noriko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
```


Pred. No.: 2.9e-156 Length: 1784
 Score: 1695.00 Matches: 312
 Percent Similarity: 98.7% Conservative: 2
 Best Local Similarity: 98.1% Mismatches: 4
 Query Match: 51.0% Indels: 0
 DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-1 (1-1784)
 QY 1 MetAsn**ValThrIleGlnTrpAspAlaValIleAlaLeuTyrlleLeuPheSerTrp 20
 Db 98 ATGATCAGGCTCACTATTCATAGGATGAGATATAGCCCTTTCATACACTTCAGCTGG 157
 QY 21 CysHlsqlyyllethrAenlleaenCysSerGlyHlsileTrpValGluProAlaThr 40
 Db 158 TGTATGAGAGAAATTAACAATATAACTGCTGCGCACTGCGTGAACAGCACA 217
 QY 41 IlePheLeuMetGlyMetLeuIleSerlleTyrcysGlnIleAlaIleValAsnGlyGln 60
 Db 218 ATTTTAAAGAGGGTGAATATCTATATATGCGCAAGCAATTAAGAACTGCGCAA 277
 QY 61 ProArgIleuHlsPheTyrlleAsnGlylleGlyGluArgPheGlnIleThrArgIle 80
 Db 278 CCAAGAAACTTCACTTTTAAATAATGGCATCAAGAAAGATTTCATATCAAGAGATT 337
 QY 81 AsnIleThrThrAlaIleGluTrpTyrlleAsnPheLeuGluProHlsAlaSerMetTyrl 100
 Db 338 AATTAACAACAGCTCGCTTGTATTAATAAACTTCGGAACCACTGCTTCTATGTAC 397
 QY 101 CysThrIleGluCysProIleHlsPheGlnIleLeuIleCysGlyIleValAsnIleSer 120
 Db 398 TGCACTGCTGAATCTCCAAACATTTTCAAGAGCACTGATATGGAAGAAAGACATTCT 457
 QY 121 SerGlyTyrlleProAspIleProAspGluValThrCysValIleTyrlleGlyTyrlleSerGly 140
 Db 458 TCTGATATTCGCGCAAGATATTCGATGAAGTAACTGTGCTATTTATGATATTCAGGC 517
 QY 141 AsnMetThrCysThrTrpAsnAla***LysLeuThrTyrlleAspThrTyrlleValVal 160
 Db 518 AACCTGACTGCACTGGAATGCTGGAAGCTCACTCACTAAGCAACAATAATAGTGTA 577
 QY 161 HisValIleSerLeuGluIleGluGluGluGluGluGluGluGluGluGluGluGluGlu 180
 Db 578 CATGTGAAGAGTTTGAAGACAGAAAGAGAGCAAGATTCACCTCAAGCTAATATTAAC 637
 QY 181 IleSerThrAspSerLeuGlnGlyIleLysIleTyrlleValIleTrpValGlnAlaIleAsn 200
 Db 638 ATCTCCACTGATTCATTAACAAGTGGCAAGAAAGTACTTGTGGTCCAAAGCAGCAAC 697
 QY 201 AlaLeuGlyMetGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 220
 Db 698 GCACCTAGGCACTGGAAGAGTCAAAACAATGCAAACTGCACTGATATGATGATCTT 757
 QY 221 SerIleAlaValIleSerArgAlaGluThrIleAsnAlaThrValProIleValIle 240
 Db 758 TCTCAGCGCTCATTTCCAGGCTGAGACTATTAATGCTACAGTCCCAAGCACTAAT 817
 QY 241 TyrTrpAspSerGlnThrTrpIleGluLysValSerCysGluMetArgTyrlleAlaThr 260
 Db 818 TATTGGATAGTCAACAACAATTGAAGAGTTTCTGTGAAATGAGATTCAGGCTACA 877
 QY 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrlleGlnIleSer 280
 Db 878 ACAACCAAACTTGAATGTAAAGAAATTTGACCAATTTTACATATGTCACACAGTCA 937
 QY 281 GluPheTyrlleGluGluProAsnIleLysTyrlleValIleGlnValLysGlyGlnIleGlu 300
 Db 938 GAATTCATCTTGGAGCCAAACATTAAGTACTATTTCAAGTGAAGATGCAAGAAACAGGC 997
 QY 301 LysArgTyrlleTrpGlnProTrpSerSerProPhePheIleLysThrProGluThr 318
 Db 998 AAAAGTACTGCGAGCTTGGAGTTCACTGTTTTTTCATATAAACCTGGAACA 1051

RESULT 6
 US-11-274-375-23
 ; Sequence 23, Application US/11274375
 ; Publication No. US20060106201A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatengu
 ; APPLICANT: Yasushi, Noriko
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105U51
 ; CURRENT APPLICATION NUMBER: US/11/274,375
 ; PRIORITY FILING DATE: 2005-11-14
 ; PRIORITY APPLICATION NUMBER: US/10/105,930
 ; PRIORITY FILING DATE: 2002-03-25
 ; PRIORITY APPLICATION NUMBER: PCT/JP00/06654
 ; PRIORITY FILING DATE: 2000-09-27
 ; PRIORITY APPLICATION NUMBER: JP 2000-240397
 ; PRIORITY FILING DATE: 2000-08-03
 ; PRIORITY APPLICATION NUMBER: JP 11-273358
 ; PRIORITY FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 360
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (140)...(295)
 US-11-274-375-23

Alignment Scores:
 Pred. No.: 6.1e-19 Length: 360
 Score: 286.00 Matches: 51
 Percent Similarity: 98.1% Conservative: 0
 Best Local Similarity: 98.1% Mismatches: 1
 Query Match: 8.6% Indels: 0
 DB: 8 Gaps: 0

US-10-667-289-2 (1-629) x US-11-274-375-23 (1-360)
 QY 267 ValIleGluPheAspThrAsnPheThrTyrlleValIleGlnIleSerGluPheTyrlleGluPro 286
 Db 140 GTTAAAGATTTTGAACCAATTTTACATATGTGCAACAGCAAGATTTCTAGAGCCA 199
 QY 287 AsnIleTyrlleValPheGlnValLysGlyGlnIleThrGlyLysArgTyrllePro 306
 Db 200 AACATTAAGTACGATTTCAAGTGAATGTCAGAAACAGCAAGGTAAGTCTGAGCCT 259
 QY 307 TrpSerSerProPhePheIleLysThrProGluThr 318
 Db 260 TGAAGTCACTGTTTTTTCATATAAACCTGGAACA 295

RESULT 7
 US-11-266-748A-33208
 ; Sequence 32008, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnson, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266,748A
 ; PRIORITY FILING DATE: 2005-11-03
 ; PRIORITY APPLICATION NUMBER: EP 04105479.2
 ; PRIORITY FILING DATE: 2004-11-03
 ; PRIORITY APPLICATION NUMBER: EP 04105482.6
 ; PRIORITY FILING DATE: 2004-11-03
 ; PRIORITY APPLICATION NUMBER: EP 04105483.4
 ; PRIORITY FILING DATE: 2004-11-03
 ; PRIORITY APPLICATION NUMBER: EP 04105507.0
 ; PRIORITY FILING DATE: 2004-11-03

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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32008
; LENGTH: 4040
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-32008

Alignment Scores:
Pred. No.: 1,44e-10 Length: 4040
Score: 216.00 Matches: 75
Percent Similarity: 41.6% Conservative: 57
Best Local Similarity: 23.7% Mismatches: 131
Query Match: 6.5% Indels: 54
DB: Gaps: 13

US-10-667-289-2 (1-629) x US-11-266-748A-32008 (1-4040)
QY 32 G|H|s|l|e|t|p|v|a|l|g|u|p|r|o|l|a|t|t|h|l|e|p|h|e|l|y|s|e|r|c|l|y|m|e|t|a|n|l|e|s|e|r|l|e|t|y|r 51
DB 731 GGGCATGTGACTGTGAAGCCCTCCCATGTAATTTTACTTGATCCAGCTGCATAATATACA 790
QY 52 C|y|e|g|l|a|l|a|l|e|l|y|s|a|n|c|y|e|g|l|n|p|r|o|l|a|t|t|y|l|e|u|h|s|p|h|e|r|y|l|y|s|a|n|g|l|y|l|e 71
DB 791 TGC-----TCTTAAGCCGAGA----- 808
QY 72 L|y|e|g|l|u|a|r|p|h|e|g|l|n|l|e|r|a|r|g|l|e|a|n|l|y|e|r|h|r|h|a|l|a|r|g|l|e|u|r|p|y|l|y|s|--- 90
DB 809 CAAGGCGCTTTCATCTATTCACAGCGTAACAAAGTTA-----ATCCTGTACAAAGTTT 859
QY 91 -----AenPhel|e|u|g|l|u|p|r|o|h|a|l|a----- 97
DB 860 GACAGAAATATCAATTTTACCATGGCCACTCCCTCAATTCCTCAAGTCACAGGCTTCCC 919
QY 98 -----SerMet|y|r|c|y|s|t|h|r|a|l|a|g|l|u|c|y|p|r|o|l|y|h|s|p|h|e|g|l|n|g|l|u|t|h|r|l|e|u 113
DB 920 CTTGGTACAACTTGTGTCTGCAACTGGCTGT---ATCAATAGTATGAAATTCAA 976
QY 114 I|l|e|c|y|e|g|l|y|s|a|r|l|e|s|e|r|g|l|y|r|p|r|o|f|a|r|l|e|p|r|o|a|r|g|l|u|a|l|t|h|r|c|y|s 133
DB 977 ATATGTGACAGAGATCTTGTTGGTGTGCTCAGAAAGCTCAAAATTTATCTGTC 1036
QY 134 V|a|l|l|e|r|g|l|u|t|y|r|s|e|r|g|l|y|a|n|m|e|r|t|h|c|y|s|t|h|r|t|r|p|h|e|n|a|l|a|**L|y|s|l|e|u|t|h|r|t|y|r 153
DB 1037 ATACAGAAAGGAGAAACGAGGACGTGGCTGCACCTGGAGAAAGAGACGACACCCAC 1096
QY 154 I|l|e|a|s|p|h|r|l|y|r|v|a|l|l|a|l|s|e|r|l|e|u|t|h|r|g|l|u|g|l|u| 170
DB 1097 TTTATACCTAGATTTACTTACAGCTTAAGTACCAAAATTTTAACTGGCAGAACCA 1156
QY 171 G|l|n|g|l|n|t|l|e|u|h|r|s|e|r|t|y|r-----I|l|e|a|n|l|e|s|e|r|h|t|a|r|s|e|r|l|e|u 186
DB 1157 TGTAAAGACATTTATTTGACTATTGACTTGGACTTGGATTCACCTGACCCCGAATCACT 1216
QY 187 G|l|n|g|l|y|l|y|s|l|y|r|l|e|u|v|a|l|t|r|p|v|a|l|l|a|l|a|n|a|l|e|u|g|l|y|e|r|l|e|u 206
DB 1217 GAA-----TCCATTTTACAGCCAGGAGTTACTGCTGTCAATAGCTCTTGAAGCTCTCT 1270
QY 207 S|e|r|l|e|u|g|l|n|l|e|h|l|e|u|a|r|p|l|e|v|a|l|l|e|r|o|s|e|r|a|l|a|l|a|v|a|l|l|e|s|e|r 226
DB 1271 TCACTTCATCCACATTCACATTTTGGACATAGTAGGCTCTCTCCCTCCGAGGACAT 1330
QY 227 A|r|g|a|l|g|l|u|r|h|l|e|a|n|a|l|a|r|h|v|a|l|p|r|o|l|y|r|h|l|e|r|l|e|r|y|r|p|a|r|s|e|r|g|l|n|t|h|r 246
DB 1331 AGAATCAAAATTTCAAAAGGCTTCGTCGAGACAGATGATCACTTATTTGAGAGATGAGGA 1390

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QY 247 T|h|r|e|g|l|u|b|v|a|l|s|e|r|c|y|s|g|l|u|e|r|a|r|g|l|y|l|a|l|a|r|h|r|h|a|n|g|l|n|h|r|t|r|p|a|s|n 266
DB 1391 CTGGTA-----CTGCTTATTCAGCTCAGATATCGGCCAGTAAACAGACAGGCTCTGGAT 1444
QY 267 V|a|l|l|e|g|l|u|b|e|a|r|h|p|h|r|a|n|p|h|e|r|h|r|t|y|r|v|a|l|-----G|l|n|g|l|n|s|e|r|g|l|u|b|h|r|l|e|u 284
DB 1445 ATG-----GTTAATGTTACAAAGCCAAAGAGACATGATTTGCTGGATCTG 1492
QY 285 G|l|u|p|r|o|a|n|l|e|y|r|t|r|v|a|l|p|h|e|g|l|n|v|a|l|r|c|y|e|g|l|n|-----G|u|t|h|r|g|l|y|l|y|e|r|t|y|r 303
DB 1493 AAACCATTTACAGAAATTTGAATTTTCAGATTTCTCTTAAGCTACATCTTTATATAGGAAGT 1552
QY 304 T|r|p|l|n|p|r|o|t|r|p|s|e|r|p|r|o|p|h|e|h|l|e|l|y|r|h|t|r|p|r|o|g|l|u|r|h|r|v|a|l|p|r|o 320
DB 1553 TGGAGTCATTTGAGCTGATGATTCATTTAGAGACACAAACACCAAGAAAGAGCT 1603

RESULT 8
US-11-266-748A-28955
; Sequence 28955, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OR INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28955
; LENGTH: 3085
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-28955

Alignment Scores:
Pred. No.: 4.78e-10 Length: 3085
Score: 209.00 Matches: 172
Percent Similarity: 32.7% Conservative: 118
Best Local Similarity: 19.4% Mismatches: 276
Query Match: 6.3% Indels: 320
DB: Gaps: 44

US-10-667-289-2 (1-629) x US-11-266-748A-28955 (1-3085)
QY 4 V|a|l|t|h|r|l|e|g|l|n|t|r|p|a|r|a|l|a|l|l|e|u|t|y|r|l|e|u|h|p|h|e|r|t|r|p|c|y|h|l|e|g|l|y 23
DB 259 TTAGCGTTGACAGACTGGGATGCAAGCTTGTATTTCTTCTCAACCTGATATACA 318
QY 24 G|l|y|l|e|h|r|a|n|l|e|a|n|c|y|s|e|r|g|l|y|h|s|l|e|r|p|v|a|l|g|l|u|r|p|r|o|l|a|r|h|l|e|h|e|l|y|s 43
DB 319 GGTGAACCTTACATCCATTT---GGTTATATCAAGTCCTGAA---TCTCCAGTTGTACAA 372
QY 44 M|e|c|l|y|e|r|a|n|l|e|s|e|r|l|e|r|t|y|r|c|y|s|g|l|n|a|l|a|l|l|e|y|s|a|n|c|y|e|g|l|n|p|r|o|a|r|g|l|y|s 63

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Db      373  CTTCATTCATTAATTCACGCGAGTTTGT-----GTGCTAAAGGAAAAATGATGATTAT 426
Qy      64  LeuHisPheTyrLysAsnGlyLe-----LysGlu 73
Db      427  TTTCATGTAATTAATGCTTAATTAATGCTTCGAAAAACAACATTACTATTCCTTAAGGAG 486
Qy      74  ArgPheGlnIleThrArgIleAsnLysThrThralaArgLeuTyrLysAsnPheLeu 93
Db      487  CAATATATCTATC-----ATTAACAGAAACGACATCCAGTGCACCTTACAGATATAGCT 540
Qy      94  GluProHisalaSerMetTyrCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113
Db      541  TCATTAATATTCGCTTCACCTTCGACACATTCCTTAACATTCGACAGCTTGAAACGAAT--- 597
Qy      114  IleCysGlyLysAspIleSerSerGlyTyrProPheAspIleProAspGluValThrCys 133
Db      598  GTTATATGAATCACAATTAATTCAGGCTTCCTCCAGAAAAACCTTAATAATTTGAGATTGC 657
Qy      134  ValIleTyrGluTyrSerGlyAsnMetThrCysThrTyrAsnAla**LysLeuThrTyr 153
Db      658  ATTGTGACAGAG---GGGAGAGAAAAAGGTGAGTGGATGGATGGATGGAGGAGAAACACAC 714
Qy      154  IleAspThrLysTyrValValHis----- 161
Db      715  TTGAGACAAACTTCACCTTAAATCTGAATGGGCAACACACAGTTGCTGATTGCAAA 774
Qy      162  ---ValLysSerLeuGluThrGluGluGluGlnGlnIleThrLeuThrSerSerTyrIleAsn 180
Db      775  GCAAACAGTGACACCCCACTTCACGCTGCTGATTAATTCCTGCTGCTGATTTGTCAAC 834
Qy      181  IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGlnAlaIleAsn 200
Db      835  ATTGAA-----GTCGCGTAGAAGACGAGACAT 861
Qy      201  AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisIleLeuAspAspIleVal----- 218
Db      862  GCCCTTGGAAGGTTACATCAGAT-----CATATCAATTTTGTTCCTGATATATTAAGTG 915
Qy      219  -----IleProSerAlaIleValIleSerArgIleGluThrIleAsnAlaThrVal 235
Db      916  AAGCCCAATCGCCACATTAATTTATCACTGATCACTCAAGGAACTGCTAGATCTTA 975
Qy      236  ProLysThrIleIleTyrTyrAspSerGlnThr-----ThrIleGluLysValSerCys 253
Db      976  AAATGACA-----TGACCAACCAAGATTAAGAGTGTATTAATCTAAATATAT 1026
Qy      254  GluMetArgTyrLysAlaThrThrAsnGlnThrTyrPhe---ValLysGluPheAspThr 272
Db      1027  AACATTCATATATGACCAAAAGATGCTCACTTGAGGCCAGATTCCTCTCGAAGACACA 1086
Qy      273  AsnPheThrTyrValGlnGlnSerGluPheTyrLeuGluProAsnIleLysTyrValPhe 292
Db      1087  GCATCCACCCGATCTTCATTCACCTGTCACAGACCTTAACCTTTTACAGAAATATGTTT 1146
Qy      293  GlnValAlaArgCys---GlnGluThrGlyLysArgTyrTyrGlnProTyrSerSer----- 309
Db      1147  AGCATTCGCTGTATGAAGAGATGTAAGGATATCTGAGATGATCGAGTGAAGAGACA 1206
Qy      310  -----ProPhePheHisLysThrPro 316
Db      1207  AGTGGATCACTATGAAGATAGACATCTAAAGCACCAGTTCGTGTATTAATAATAGAT 1266
Qy      317  -----GluThrValPro----- 320
Db      1267  CCATCCCATACTCAAGGCTACAGACCTGTACACTCGTGTGAGAAACATTCCTCTCTTTT 1326
Qy      321  GlnValThrSerLysAlaPheGlnHisAspThr-----TyrAsnSerGlyLeu 336
Db      1327  GAAGCCATGGAAGAAATCTTGATGATGAAGTGACTGCACAAATGGAATTCACATTTA 1386
Qy      337  -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352

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Db      1387  CAAATTTACACAGTTAATGCCACAAAACGACAGTAATCTCAAAATGATGCC----- 1440
Qy      353  AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372
Db      1441  -----TATCTAGCAACCTTAACGTAAAGAAATCTT 1470
Qy      373  IleGlyIlePheAsn----- 377
Db      1471  GTTGGCAATACAGATCAGCTGTTTAATCTATCCTGCTGCTGATGACTTTCAGGTACTCAC 1530
Qy      378  -----ArgSerPhe----- 380
Db      1531  CCTGTAATGATCTTAAGCATTCCTCCCAAGATTAACATGCTTTGGTGGATGAGACTACT 1590
Qy      381  ---ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrLeuTyrGluAsp 399
Db      1591  CCAAGGAATCTGTAAAGAAATATATATCTT-----GAGTGGTGT----- 1629
Qy      400  IleProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeu--- 418
Db      1630  GTGTTATCAGATTAAGACACCTGTATACACAGACTGGCAACAGAGATGATGATCCGTGCAT 1689
Qy      419  -----MetAsnAsnAsnSerSerGluGlnValLeuTyr-----ValAspPro 432
Db      1690  CGCACTTATTTAAGAGGAACTTAGCAGAGAGCAAAATGCTTGTGATTAACAGTTACTCCA 1749
Qy      433  MetIleThrGlu-----IleLysGluIlePhe 441
Db      1750  GTATATGCTGATGAGACCAAGAACCTCGTAATCCATAAAGCATACCTTAACAGACT--- 1806
Qy      442  IleProGluHisLysProThrAspTyrLysLys-----GluAsnThrGlyProLeu 458
Db      1807  CCACCTTCCAAAGACCTACTGTTGCGACAAAAGTAGGAGAAAACGAAAGCTGTCTTA 1866
Qy      459  GluThrArgAspTyrPro-----GlnAsnSerLeuPheAspAsnThrThrValVal 475
Db      1867  GAGTGGACCAACTCTCTGTGATGTTCAGAAATGATTAATTCAGAAATTAATTAATTTT 1926
Qy      476  Tyr----- 476
Db      1927  TATTAAGAACATCATTTGGAATTAAGAACTGCTGTGAATGTGATTCCTCCACAGAAATAT 1986
Qy      476  ----- 476
Db      1987  ACATTCCTCTTGTGACTAGTGAACATTTGATGATGATGATGATGATGATGATGATGATGAT 2046
Qy      476  ----- 476
Db      2047  GAAGTGGAGAGATGCTCCAGAAATTCATTTACTACCCCAAGTTTGCTCAAGAGAA 2106
Qy      476  ----- 476
Db      2107  ATTGAAGCATATGTCGTGCTGTTGCTTAGCATTCCTATTAGCAACTCTTCGGAGATG 2166
Qy      477  -----IleProAsp 479
Db      2167  CTGTTCTGTTTATAAGACAGACTTAATTAACAAACATCTGGCTTAATGTTCCAGAT 2226
Qy      480  LeuAsnThrGlyLysProGlnIleSer-----AsnPheLeu 492
Db      2227  CTTCAAGAGATATATGTCCTCAGGTGTCACTTCACCTCCCAAGGACCAATTTAAT 2286
Qy      493  ProGluLysSerHisLeuSerAsnAsnAsn-----GluIleThr 505
Db      2287  TCAAAAGATCAAAATGATTAATGATGCGCAATTTCACTGATGCTAATGTTGGAATAGAA 2346
Qy      506  SerLeuThrLeuLysPro---ProValAsp---SerLeuAsp----- 517
Db      2347  GCAAATGACAAAAGCCTTTTCCAGAAAGATCTGAATCATTTGACCTGTTCAAAAAGAA 2406
Qy      518  -----SerGlyAsnAsnProAspLeuGlnLys 526
Db      2407  AAAATTATATCTGAAGAGACACAGCACTGTGATTTGGGGGGCTTCATGATGATCTTCT 2466

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Db 259 TTGAGCTTGCAACCTTGCGTAGTCGAAAGCCTTGTTATTCTTCTCCACCACTGAATCTACA 318

Qy 24 GilyllIethrasnilleasnCyseRglYhiSllIetrPvalGluProIalathrlIephelys 43

Db 319 GGTGAACCTTCTAGATCCAACTGT---GGTATATACAGTCCGAA---TCTCCAGTGTGACA 372

Qy 44 MetGlyMetAsnIleSerIleTyrCyseGlnIalIalIeIyAsnCyseGlnProIaRglys 63

Db 373 CTTCATCTTAATTTCACTGCACTGTTGT-----GTCCTAAAGAAAAATGATGATTTAT 426

Qy 64 LeuHlsphetyrLyAsnGlyIle-----LysGlu 73

Db 427 TTTCAATGTAATGCTAAATTAATTAATTCATGCGAAACAAACCATTTTACTATTCTTAAGAG 486

Qy 74 ArgphelGlnIleThrArgIleasnlysrThrIalabgLeuTrpYrlyAsnPhelou 93

Db 487 CAATGTACTATC-----ATMAACAGAACAGCATAGTGCACCTTTACAGATATAGCT 540

Qy 94 GluProHlsAlaSerMetYrCyseThrIaGluCyseProIyHlsphelGlnIuThrleu 113

Db 541 TCATTAATTAATTCACACTCTTCCAACTCTTAATTCATTCGGACAGCTTGACAGAT--- 597

Qy 114 IleCyseGlyLyAspIleSerSerGlyYrProProAspIleProAspGluValThrCyse 133

Db 598 GTTATGTGAATCACAATATATTTCAAGCTTGCTCCAGAAAACCTMAAATTTGAAGTTGC 657

Qy 134 ValIleYrGluYrSerIlyAsnMetThrCyseThrTPAsnAla**LysleuThrYr 153

Db 658 ATTTGAAACGAG---GGAGAGAAATAGAGTGTGAGTGGAGTGGAGGAGAAACACAC 714

Qy 154 IleasrThrLytrValValHls----- 161

Db 715 TTGGAGCAAACTTCACTTAATAACTGAATGGCAACACAACTTTCGTATTCGAAA 774

Qy 162 ---ValLyseSerLeuGlnThrGluGluGlnGlnIYrLeuThrSerSerYrIleasn 180

Db 775 GCAAAACGAGACACCCCACTCATGCACTGTGATTAATTTACTGTGATTTGTCAAC 834

Qy 181 IleserThrAspSerLeuGlnGlyGlyLybYrYrleuValTPValGlnIalalaaan 200

Db 835 ATTTGAA-----GTCTGGTATAAGCAGAGAAAT 861

Qy 201 AlaIeugIyMetGluGluSerLyseGlnIeugGlnIleHlsIleAspAspIleVal----- 218

Db 862 GCCCTTGGGAAGGTTACATCAGAT-----CATATCAATTTTGATCCTGTATATAAAGTG 915

Qy 219 -----IleProSerAlaIalValIleSerArgIalGluThrIleasnIalThrVal 235

Db 916 AAGCCCAATCCGCGCACATTAATTTACAGATGATCACTACAGAGAACTGCTGTATCTTA 975

Qy 236 ProIySrThrIleIleYrTPAspSerGlnThr-----ThrIleGluYsValSerCyse 253

Db 976 AAATTTGACA-----TGAACCAACCAACCAATTAAGAAGTGTATTAATTAATTAAT 102

Qy 254 GluMetArgYrLyValalathrThraasnGlnThrTPAsn---VallyseGluPheAspThr 272

Db 1027 AACATTCATATAGAACCAAGAAGATGCCCACTCTTGAGCAGAGATTCCTCTGAAGACACA 108

Qy 273 AsnPhetThrYrValGlnGlnSerGluPheYrLeuGluProAsnIleYrYrValPhe 292

Db 1087 GCATCCACCCGATCTTCATCACTGTCGCAAGACCTTAAACCTTTTACAGAAATGTGTT 114

Qy 293 GluValaLyCyse---GlnGluThrGlyLyAspArgYrTPGlnProTrpSerSerProPhe 311

Db 1147 AGGATTCCTGTATAGAAAGATGATGTAAAGGATCTCGAGTGCATCGAGTGAAGAAGACA 120

Qy 312 PheHlsYrThrProGlu---ThrValPro-----GlnValThrSerYrlyAlaPheG1 328

Db 1207 AGTGGATCACTATAGATGAATACATTCCTCCTTTTGAAGCCAAATGAAAATCTGGA 126

Qy 328 nhIlaasrThr-----TPAsnSerGlyLeu-----ThrVal---AlaSe 340

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Db      1267 TTATGAGTCACTCTCAAGATGAAATCATTTTCAAAATTACACAGTTAATGCCAC 1326
Qy      340 rIleSerThrGlyHisIleuThrSerAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMe 360
Db      1327 AAAACGACAGTAATCTTCACAAATGATCCG----- 1357
Qy      360 tIleValPheAlaValMetLeuSerIleLeuSerIleGlyIlePheAsn----- 377
Db      1358 -----TATCTACCAACCTTAACAGTAAGAAATCTTGGCAATACAGATGACGCTGT 1410
Qy      378 ----- 380
Db      1411 TTTAATATCTCCCTGCTGTGACTTTCAAGCTACTACCCCTGTAATGATCTTAAAGCAATT 1470
Qy      380 e-----ArgThrGlyIleLysArg 387
Db      1471 CCCCAAGATTAACATGCTGTTGGGTGAATGACACTTCCAAAGGAATCTGTAAAGAAATA 1530
Qy      387 gIleLeuLeuLeuIleProLysTrpLeuTrpGluAspIleProAsnMetLysAsnSerAs 407
Db      1531 TATACTT-----GAGTGGTGT-----GTGTTATCAGATTAAGCACCCCTG 1569
Qy      407 nValValLysMetLeuGlnGluAsnSerGluLeu-----MetAsnAsnAsn 423
Db      1570 TATCACAGACTGCGACACAGAAAGATGGTACCGCTGATCGACCTATTATAGAGGAACCTT 1629
Qy      423 rSerGluGlnValLeuTrp-----ValAspProMetIleThrGlu----- 436
Db      1630 AGCAGAGAGCAAAATGCTATTGATACAGTTACTCCAGTATATCTGATGACCAAGAG 1689
Qy      437 -----IleLysGluIlePheIleProGlnHisLysProThrAs 449
Db      1690 CCCTGAATCCATAAGCATACCTTAAACAAGCT-----CCACCTTCCAAAGACCTACTGCT 1746
Qy      449 pTyLysLys-----GluAsnThrGlyProLeuGlnThrArgAspTrpPro----- 464
Db      1747 TCGACAAAAAAGTAGGAAAAAGAAAGAAAGCTGCTCTTGAAGGAGCAACTTCTGTTGA 1806
Qy      465 -----GlnAsnSerLeuPheAspAsnThrValValValTrp----- 476
Db      1807 TGTTCAGATGATGATTTATCAGAAATTAATATATTTTATGAACCATATTGAAATGA 1866
Qy      476 ----- 476
Db      1867 AACTGCTGTGATGTGATTTCTCCACACAGAAATATATATTGCTCTTGAAGTGA 1926
Qy      476 ----- 476
Db      1927 CACATTTGACATGATGACAAATGAGACATACACAGATGAGTGGAGAGATGCTCCAGA 1986
Qy      476 ----- 476
Db      1987 ATTCACTTTACTACCCAAAGTTTGTCAAGAGAAATTGAAGCATATGCTGCTGT 2046
Qy      476 ----- 476
Db      2047 TTGCTTAGCATTCCTATTGACAACTCTTCTGAGATGCTGTTCTGCTTAAATAAGCAGA 2106
Qy      477 -----IleProAspLeuAsnThrGlyTrpLysProG 487
Db      2107 CCTAATTAATAAACACATCTGGCTTAATGTTTCAGATCTCTTCAAAAGTCAATATGCCCCA 2166
Qy      487 nIleSer-----AsnPheLeuProGluGlySerHisLeuSerAs 500
Db      2167 GTGCTCACCTCACTCTCTCAAGGACAAATTTTAATTCAAAAGATCAAATGTAATCCAGA 2226
Qy      500 nAsnAsn-----GluIleThrSerLeuThrLeuLysPro--Pr 512
Db      2227 TGGCAATTTCACTGATGTAAGTGTGTGGAATATGAGCAATGACAAAAAGCCTTTTCC 2286
Qy      512 oValAsp-----SerLeuAsp----- 517
Db      2287 AGAAGATCTGAATCATTTGACCTGTTCAAAAAGAAAAAATTAAATACTGAAGACACAG 2346

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Qy      518 -----SerGlyAsnAsnProArgLeuGlnLysHisProAsnPheAlaPheSerVal 534
Db      2347 CAGTGGATATGGGGGGGCTTCATGATGATCATCTTCTAGGCGCAAGCATTTCTAGCAGTGA 2406
Qy      534 lSerSerValAsnSerLeuSerLeuSerLeuThrIlePheLeuGlnGluLeuSerIleLeuAs 554
Db      2407 TGAATATGAACTCTTCA-----CAAAACACTTCGACACCTGCTCCAGTATTTCAACCGTGAC 2463
Qy      554 nGlnGly-----GluCysSerSerProAspIleGln-----AsnSerValGluGluThrTh 572
Db      2464 CAGTGGCTACAGACACCAAGTTCCGTCAGTCAGTCAGTCTTCAAGATCCAGTCTACCCA 2523
Qy      572 rMetLeuLeuGluAsnAspSerProSerGluThrIleProGlnGlnThrLeuLeuProAs 592
Db      2524 GCCCTGTGTAGAT-----TCAGAGAGCGCGCGAAGAGATCTACAAATTAGTAGA 2571
Qy      592 pGluPheValSerCysLeuGlnGlyIleValAsnGlnGluLeuProSerIleAsnThrTrp 612
Db      2572 TCATGTAGATGGCGGTGATGTATTTTGGCCAGGCA-----CAGTACTT 2616
Qy      612 eProGlnAsnIleLeuGlu-----SerHisPheAsnArg 623
Db      2617 CAAACAGAACTGCAGTCAGTCAGATCCAGTCCAGATATTTCACATTTTGAAG 2671

RESULT 10
US-11-330-726-179
: Sequence 179, Application US/11330726
: Publication No. US20060204982A1
: GENERAL INFORMATION:
: APPLICANT: Engelhard, Eric
: APPLICANT: Morris, David
: TITLE OR INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
: FILE REFERENCE: 20366-011002
: CURRENT APPLICATION NUMBER: US/11/330,726
: CURRENT FILING DATE: 2006-01-12
: PRIOR APPLICATION NUMBER: US 10/052,482
: PRIOR FILING DATE: 2001-11-08
: PRIOR APPLICATION NUMBER: US 09/747,377
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US 09/798,586
: PRIOR FILING DATE: 2001-03-02
: NUMBER OF SEQ ID NOS: 241
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 179
: LENGTH: 2723
: TYPE: DNA
: ORGANISM: Homo sapiens
US-11-330-726-179

Alignment Scores:
Pred. No.: 2,93e-08 Length: 2723
Score: 190.00 Matches: 144
Percent Similarity: 34.7% Conserved: 82
Best Local Similarity: 22.1% Mismatches: 228
Query Match: 5.7% Indels: 197
DB: Gaps: 35

US-10-667-289-2 (1-629) x US-11-330-726-179 (1-2723)
Qy      104 GluCySerProLysHisPheGlnGluThrLeuIleCysGlyLysAspIleSerSerGlyTrp 123
Db      272 GAAGGACGACCAATGAAAGAAATGATGCGATCGCAACCGTTTCACTCTGCTACTTTT 331
Qy      124 ProProAspIleProAspGluValThrCysValIleTrpLys----- 137
Db      332 TTCACACCTGCTCTCTGATGACAGTAACTCTCGGAAACCTGAGATCTTAAATG 391
Qy      138 ---TyrSer-----GlyAsnMet-ThrCysThrTrpAsnAla**LysLeuThrTrp 154
Db      392 TCGTCTCCCAATAGAAACATTCACCTCTGTGTGAAGCCGTGGACAAATGAGAGACT 451
Qy      154 eAspThrLysTrpValValHisValLysSerLeuGluThrGlnGluGlnGlnTrpLe 174

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; NUMBER OF SEQ ID NOS: 1441
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 109
 ; LENGTH: 2736
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-669-920-109

Alignment Scores:

Pred. No.:	2,95e-08	Length:	2736
Score:	190.00	Matches:	144
Percent Similarity:	34.7%	Conservative:	82
Best Local Similarity:	22.1%	Mismatches:	228
Query Match:	5.7%	Indels:	197
DB:	6	Gaps:	35

US-10-667-289-2 (1-629) x US-10-669-920-109 (1-2736)

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Qy 104 GluCysProlyshisphengluThrlleuileCysglYlysaspIleSerSerGlyTyr 123
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    |||
Db 285 GAAGGACAGCCAAACATGAAGAAATGCGCATCTGCAACCGTTTCACTGCTACTTTT 344
    |||
    |||
    |||
Qy 124 ProProaspIleProaspGluValThrcysValileTyrGlu----- 137
    |||
    |||
    |||
Db 345 TCTCAACACCTGCTCTGAAATGACAGTTACTCTCGAAAACCTGAGATCTTTAAATG 404
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    |||
    |||
Qy 138 ---TyrSer-----GlyAsnMet-ThrCysThrTyrAsnAla**LysLeuThrTyr11 154
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    |||
Db 405 TCGTCTCCCAATAAGAAACATTCACCTGCTGTGAGAGCGCTGGACAGATGGAGAGACT 464
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Qy 154 eAepThrLysTyrValValHisValLysSerLeuGluThrgluGluGluGlnTyrLe 174
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    |||
    |||
Db 465 TCCTACCAATATAT-----TCACACTTACCAAGGAGAGAGAGAGAGACT 509
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    |||
Qy 174 u-----ThrsSerTyrIleAsnIleSerThrsAspSerLeuGlnGlyLysly 191
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Db 510 CATGCATGATGTCACAGTACATACCGGTCGCCCACTCTGCCACTTTGGCAAGCA 569
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Qy 191 s-----TyrLeuValTyrValGlnAlaAlaAlaAlaAlaAlaAlaAlaAla 204
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    |||
Db 570 GTACACCTCCATGTCGAGACATATCATGATGATGTAATGCCACTAACAGATGGAGAG 629
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Qy 204 tGluGluSerLysGlnLeuGlnIleHisLeuAspAspIleValIleProSer----- 221
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    |||
Db 630 CAGTTCTCGGATGAACCTTATGTGACGTGACTTACATGTTACGACGACCCCTCTT 689
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Qy 222 -----AlaAlaValIleSerArgAlaGluThrlleAsnAlaThrValProLysThr11 239
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    |||
Db 690 GGAAGCTGGCTGTGAAGTAAACAGCCAGAAC-----AGAAAACTCTACTGTG 740
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    |||
Qy 239 eileTyrTyrAspSerGlnThrThrlleGlu-----LysValSerCy 253
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Db 741 GATTAAATGTCCTCACCTACCTGATTTGACTTTAAAACTGGTTGCTTACCGCTCTGTA 800
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Qy 253 eGluMetArgTyrLysAlaThrThraAsnGlnThrTyrAsnValLysGluPheAspThrAs 273
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Db 801 TGAATATCGATTAAACCCGAGAAAGCAGTGAAGTGGAGATC-----CA 845
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    |||
Qy 273 nphethrTyrValGlnGlnSerGluPhe-----TyrLeuGluProAsnIleLysTyr 290
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    |||
Db 846 TTTTGTCT--GGGACGAAACAGAGTTTAAGATTCTACGCTTACATCCAGACAGAAATA 902
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Qy 290 rValPheGlnValArgCysGlnGluThrglyLysArgTyrTyrGlnProTyrPheSerSerPr 310
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    |||
Db 903 CCTGTGTCAAGTTCGCTGC--AAACGACACATGATATCTGAGATGATGATGAT----- 954
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    |||
Qy 310 oPhePheHisLysThrProGluThrValProGlnValThrseryLysAlaPheGlnHisAs 330
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    |||
    |||
Db 955 -----CCAGCGACCTTCATTCAGATACCTAGTACCTTACCATGAAATGA 998
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Qy 330 pThr-----TyrAsnSerGlyLeuThrValAlaSerIleSerThrglyHisLeuThrse 348
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Db 999 TACAACCGGTGG-----ATCTCTGTGGCTGTCTTCT----- 1032
  
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Qy 348 rAspAsnArgGlyAspIleGlyLeuLeuGlnMetIleValPheAlaValMetLeuSe 368
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    |||
Db 1033 -----CGTGCATCTGTGTTGATATATGTCGGGACGAGCTTTGAA 1073
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Qy 368 rIleLeuSerLeuIle-----Gly11 375
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Db 1074 GGGCTATATGATATGATGACCTGATCTTTCCGACAGTCTCTGGCCCAAAATAAAGATT 1133
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    |||
Qy 375 ePheAsnArgSerPheArgThrglyLysArgArgIleLeuLeuLeuIle----- 392
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    |||
Db 1134 TGATGCTCATCTGTGGAAGAGGCAAGTGTGAAGAACTACTAGTCCCTTGGAGTCCA 1193
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    |||
Qy 393 -----ProLysTyrLeuTyrGluAspIleProAsnMetLysAsnSerAsnValVa 409
    |||
    |||
    |||
Db 1194 AGACTTCTCTCCACCTTCTGATATGAGACTTG-----CTGGT 1232
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    |||
Qy 409 lLysMetLeuGln-----GluAsnSerGluLeuMetAsnAsnAsnSerSerG 425
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    |||
Db 1233 GAGATATTGAAGATGATGATGATGATGAGACAGCATCTATATGTCATTCAAAAGA 1292
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Qy 425 u-----GlnValLeuTyrValAspPro----- 432
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    |||
Db 1293 ACACCCAAAGTCAAGTATGAACCCACATACCTGATCTGACACTGACGCGGAGG 1352
    |||
    |||
    |||
Qy 433 -----MetIleThrglyLysGluIlePheIleProGluHisLys 446
    |||
    |||
    |||
Db 1353 GAGCTGTGACAGCCCTTCTCTTGTGTGAAAAGTGTGAG-----GAAACCCAGGCCAA 1406
    |||
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    |||
Qy 446 eProThrAspTyr-----LysLysGluAsnThrolyProLeuG 459
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    |||
    |||
Db 1407 TCCCTCCACATTTCTATGATCTTGAAGTCAATGAGTGAAGAACGAAATCTGAAACCA 1466
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Qy 459 uThrArgAspTyrProGlnAsnSerLeuPheAspAsnThrThValValTyrIleProAs 479
    |||
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    |||
Db 1467 CACTGTGAGC-----CCCAAGTGCATTAAGCATGAAAGCAAA-----ATCCCTTA 1511
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Qy 479 pLeuAsnThrGlyTyrLys-----ProGlnIleSerAsnPheLe 492
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    |||
    |||
Db 1512 TTTTCATGCTGTGTGATTCAAATGTTCAACATGAGCCCTTACCAAGCCGACGACAA 1571
    |||
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    |||
Qy 492 uProGluGlySerHisLeuSerAsnAsnGlnIleThrsLeuThrLeuLysPro-- 511
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    |||
    |||
Db 1572 CCCGAGATCTCTTAC--CACAAATATTACTGATGTGTGAGCTGCTGTGGCCCTTGC 1628
    |||
    |||
    |||
Qy 512 -----ProValAspSerLeuAspSerGlyAsnAsnProArgLeuGlnLysHisProAs 529
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    |||
Db 1629 AGGTGCACCGGCACCTCTGTTGAATGAAGCAAGTAAAGCTTTAAATCC----- 1680
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    |||
Qy 529 nPheAlaPheSerValSerSerValAsnSerLeuSerAsnThrIlePheLeuGlyGlu 549
    |||
    |||
    |||
Db 1681 -----TTCAAACCATTAAGCTAGAGAGA 1706
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    |||
    |||
Qy 549 uSerLeuIleLeuAsnGlnGlyLysCysSerSerProAspIleGlnAsnSerValGluG 569
    |||
    |||
    |||
Db 1707 GGAAGAAAGCAACCGACGAGGAGGTGAAGAAC-----TTCATTTCTAGACCTGCA 1760
    |||
    |||
    |||
Qy 569 uGluThrThrMetLeuLeuGlnAsnAspSerProSerGluThrIleProGluGlnThrLe 589
    |||
    |||
    |||
Db 1761 GATATCGCTCTGCTGCTG-----CCCGAGAGAAAAACCCCTTTGGCTCGC 1808
    |||
    |||
    |||
Qy 589 uLeuProAspGluPheVal-----SerCysLeuGlyIleVa 601
    |||
    |||
    |||
Db 1809 TAAACCTTGATATATGATGAGATTCAAGTTCACAAAGATGATGATATCATATGCT 1868
    |||
    |||
    |||
Qy 601 l-----AsnG 603
    |||
    |||
    |||
Db 1869 ACCAAAAAGAGAGAGAAACAGCGGCAAGCCCAAGAAACCCGAGACTCTGAGAACTAA 1928
    |||
    |||
    |||
Qy 603 uGluLeuProSerIleAsnThrTyrPheProGlnAsnIleLeu-----GluSe 619
    |||
    |||
    |||
Db 1929 GGAATATGCAAGATGTCCGGGTGATGATTAACACATCTCTGTGTGGTGCAGATCC 1988
  
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Oy      619 rHiPheA5nArgleSeRleuNeuGlyUys 629
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Db      1989 ACATGTAAACAGCTGCCTTGGTAAGA 2019

RESULT 12
US-11-266-748A-29132
; Sequence 29132, Application US/11266748A
; Publication No. US20060134663AI
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: Method of Using the Same
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 29132
LENGTH: 3162
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-29132

Alignment Scores:
Pred. Score: 3.63e-08 Length: 3162
Score: 190.00 Matches: 144
Percent Similarity: 34.7% Conservative: 82
Best Local Similarity: 22.1% Mismatches: 228
Query Match: 5.7% Indels: 197
DB: Gaps: 35

US-10-667-289-2 (1-629) x US-11-266-748A-29132 (1-3162)
Oy      104 GluCyeProAlphHispehneGiunThrLeuIIEcySGILyAspRIeSerSeclYtyr 123
         :|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      301 GAAGGCCAGCCCAACAATAAGAAAATGTCGCATTCTCGAACCGTTTCACTTGACTCTT 360
Oy      124 ProProAspRIeProAspGIuValThrCyVaIIeTyrgLu----- 137
         ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      361 TGTCAACACCTGCTTCTGAATGSAAGTTACCCTCCTGAAAACTGACATTMAATG 420
Oy      138 ---TYser-----GLysenNec-ThrCYSThrTrpAnaLa**LYsLeuThrTYrII 154
         :::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      421 TCCTTCCTCCCATMATAGAAACATTCACTGCTGTGGTAGAGCCTGGACAGATGAGAGACT 480
Oy      154 eASpRIrLyTygValVAlHIsValysSerLeuGIunThrgIugluGIunGIunTYrl 174
         :|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      481 TCCTACCAATTAT-----TCACTTGACTTACCACAGGAGGAAGAGACACT 525
Oy      174 u-----THrSereTYrIIeaNIleSerThraSPseRleuGIingIygiLYsLY 191
         :|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      526 CATGCAATGAATGTCCAGACTACACTAACCGGTGAGCCCCCAAATCTCTGCACATTGGCAAGCA 585
Oy      191 s-----TYrlEuValTrpValGlndlaalaaIdaenalaLeuGIyme 204
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Db	586	GTACACCTCCAGTGGAGACATCATCATGATGGTCAATGCACCTAACAGATGGAG	645
Oy	204	tGlUGuSerlyseGlnLeuGlnIleHleuAspIleValIleProSer-----	221
Db	646	CAGTTTCCCGATGAACTTTATGTGGACGGTCACTTCACTTACCTGACGACCTCTTT	705
Oy	222	-----AlaIleValIleSerArgIleGluThrIleAsnIleThrValProlyThrIle	239
Db	706	GGAGCTGGCTGGAGATGAAACGACGAAAGAC-----AGAAAACCTTACCTGTG	756
Oy	239	eIleTyTrpAspSerGlnThrIleGlu-----LysValSerCy	253
Db	757	GATTAAATNGTCTCCACCTACCTGATTTGACTTAAACGTGGTTGTTCAAGCTCTGTA	816
Oy	253	sgIuMeuArgTyIysValaThrThrAsnGlnThrTrpAsnValLysGluPheAspThrAs	273
Db	817	TGAATTCGATTTAAACCCGAGAAAGCAGCTGAGTGGAGATC-----CA	861
Oy	273	nPheThrTyValGlnGlnSerGluPhe-----TyIeGluPProAsnIleTy	290
Db	862	TTTTGGCT---GGGAGAGCAACAGAGTTTAAAGATTCTCAGCCTTACATCCAGACAGAAATA	918
Oy	290	rValPheGlnValArgCySGlnGlnThrGlyLysArgTyTrpGlnProTyrPseSerPr	310
Db	919	CTTGTCAGAGTTGCTGC---AAACGACAGCATGAGTACCTGAGATGAGTGAAGT---	970
Oy	310	oPhePheIleLysThrProGluThrValProGlnValThrSerLysValaPheGlnHisAs	330
Db	971	-----CCAGCGACCTTCATTCAGATATCCTAGTACCTGACCATGAAATGA	1014
Oy	330	pThr-----TrpAsnSerGlyLeuThrValAlaSerIleSerThrGlyHleuThrSe	348
Db	1015	TACACCGGTGG---ATCTGTGGCTGCTGCTCT---1048	
Oy	348	rAspAsnArgGlyAspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSe	368
Db	1049	-----GCTGTCATCTGTTGATTTGTCTGGGACAGTGGCTTTGAA	1088
Oy	368	rIleLeuSerIleuLeu-----GlyIle	375
Db	1090	GGGCTATATAGCATGATGACCTGCATCTTCCGCCAGTTCTGTGGCCAAATAATAAAGATT	1149
Oy	375	ePheAsnArgSerPheArgThrGlyIleLysArgArgIleLeuLeuLeuLeu-----	392
Db	1150	TGATGCTCATGTCGTGGAGAGGCGCAAGTCTGAAGAATCACTGAGTGGCTGGAGTGC	1209
Oy	393	-----ProlysrIleuTyArgIleAspIleProAsnMetLysAsnSerAsnValVa	409
Db	1210	AGACTTCTCTCCCACTTCTGACTATGTAGAGACTTG---CTGT	1248
Oy	409	lLysMetLeuGln-----GluAsnSerGlyIleuMetAsnAsnSerSerGly	425
Db	1249	GGAATATTAGAAATAGATGATGATGAGACACAGCATCTAATGTCAAGTCATTCAAAGA	1309
Oy	425	u-----GlnValLeuTyValAspPro-----	432
Db	1309	ACACCCAAAGTCAAGTATGAAACCAACATACCTGATCTGTACACTGACTCAGCCGGGG	1368
Oy	433	-----MetIleThrGlnIleLysGlnIlePheIleProGluHisIle	446
Db	1369	GAGCTGTGACAGCCCTTCCCTTTGTGTGAAAGTGTAG---GAAACCCAGGCCCA	1422
Oy	446	sProThrAspTy-----LysLysGlnAsnThrGlyProLeuGly	459
Db	1423	TCCTCTCCACATCTCATATATCCTGAGGTCTTGAAGAACCCAGAGATCTGTAAACACCCA	1482
Oy	459	uThrArgAspTyTrpGlnAsnSerLysPheAsnThrThrValValTyIleProAs	479
Db	1483	CACCTGGAGAC---CCCCAGTGCATTAACATGAGAGGCAAA-----ATCCCTTA	1527
Oy	479	pLysAsnThrGlyTyIys-----ProGlnIleSerAsnPheIle	492
Db	1528	TTTTTCATGCTGTGGATCCAAATSTTCAACATGCGCCTTACACAGCCCAAGCCAGCA	1587


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Db      966 CCAGCATCTAATGTCAGTCATTCATAAAGAACACCAAGTACAGTATGAAACCACTA 1025
Qy      429 rValAspPro-----MetIleThrG1 436
Db      1026 CCTGATATCTGACACTGACTGAGCCGGGAGAGCTGTGACAGCCCTTCCCTTTGCTGA 1085
Qy      436 uileLysGluIlePheIleProGluHleIleProThrAspTyr-----450
Db      1086 AAATGTGAG-----GACCACCAAGCCAAATCCTCCACATTCATATGATCTGAGTCAT 1139
Qy      451 ---LysLysGluAsnThrGlyProLeuGluThrArgAspTyrProGluAsnSerLeuH 469
Db      1140 TGAGAACCCAGAGATCTGTAACACCAACCACTGGGAC---CCCGAGTCATATAGCAT 1196
Qy      469 eAspAsnThrThrValValTyrIleProAspLeuAsnThrGlyTyr-----485
Db      1197 GGAAGGCAAA-----ATCCCTATTTTCATGCTGTGATCCAAATGTTCAAC 1244
Qy      486 -----ProGluIleSerAsnPheLeuProGluIleSerHleLeuSerAsnAsn 502
Db      1245 ATGGCCCTTACCAAGCCAGCCAGACACCAAGATCTCTTAC---CACAATATTAC 1301
Qy      502 ngLileThrSerLeuThrLeuLysPro-----ProValAspSerLeuAspSerG1 519
Db      1302 TGATGTGTGAGCTGGCTGTGGGCTGAGGCTGACAGTGCACCGGCACTGTGTAATGAAGC 1361
Qy      519 yAsnAsnProArgLeuGluIleLysHisProAsnPheIlePheSerValSerSerValAsn 539
Db      1362 AGGTAAAGATGCTTAAATCC-----1383
Qy      539 rLeuSerAsnThrIlePheLeuGlyGluLeuSerLeuIleLeuAsnGlnGlyCys 559
Db      1384 ---TTCAAACCACTTAAGTTAGAGAAAGAGGAAAGCAACCAAGCAGAGGAGTGA 1439
Qy      559 rSerProAspIleGlnAsnSerValGluGluGluThrThrMetLeuLeuGluAsnAsp 579
Db      1440 AAGC-----TTCATCTCTGAGCTGACGACAGATACCGCTGGCTGCTG-----1482
Qy      579 rProSerGluThrIleProGluGlnThrLeuLeuProAspGluPheVal-----595
Db      1483 -CCCCAGAGAGAAAACCCCTTGGCTCGCTAAACCTTGGATTATGTGAGATTCAAA 1541
Qy      596 -----SerCysLeuGlyIleVal-----601
Db      1542 GGTCAACAAGATGTCATATCATTTGCTACAAACACAGAGAGAAACAGCGGCAAGCC 1601
Qy      602 -----AsnGluGluLeuProSerIleAsnThrTyrPhePr 613
Db      1602 CAAGAAGCCGGGAGCTCCTGGAACAAATTAAGAGTATGCCAAGGTGTCGGGTCATGA 1661
Qy      613 oGlnAsnIleLeu-----GluSerHisPheAsnArgIleSerLeuLeuGly 629
Db      1662 TAAACAACATCTGTGTGTGTGTCAGATCCACATGCTAATAAAACGTGGCTGCTTGAAGA 1721
Qy      629 s 629
Db      1722 A 1722

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; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patent version 3.2
; SEQ ID NO 3101
; LENGTH: 5252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-3101

Alignment Scores:
Pred. No.: 1,18e-07 Length: 5252
Score: 188.00 Matches: 109
Percent Similarity: 36.0% Conservative: 68
Best Local Similarity: 22.2% Mismatches: 184
Query Match: 5.7% Indels: 130
DB: Gaps: 26

US-10-667-289-2 (1-629) x US-10-511-937-3101 (1-5252)
Qy      111 GluThrLeuIleCysGlyLysAspIleSerSerGlyTyrProProAspIleProAspGlu 130
Db      1108 GAAGATTAACATATTGGACACCGTATTTTGTCTGAGATATCCACAGATCTCTCAACAA 1167
Qy      131 ValThrCysValIleTyrGluTyrSerGlyAsnMetThrCysThrTyrPheAsnAla**Lys 150
Db      1168 CTGAATGTGAGACACATGATTAA--GAATTTATATGATGAGATCCAGAAAGG 1224
Qy      151 LeuThrTyrIle-----AspThrLysTyrVal-----159
Db      1225 GTGACACGTTGGTGGGCGCCACGCTACACAGCTTACCTTATGTAAGTTTTCAGGA 1284
Qy      160 ---ValHisValLysSerLeuGluThrGluGluGlnGlnTyrLeuThrSerSer 177
Db      1285 AATATGTGTAGACTTAAGAGCTGAAGCACTTACAAACGAAGCTAT-----1332
Qy      178 TyrIleAsnIleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTyrValGln 197
Db      1333 -----CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1386
Qy      198 AlaIleAsnAlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspAspIle 217
Db      1387 GCTCAACATCCGCTGGTGCATCATCAATCAATTTTA---GTTAATATATGAGAA 1443
Qy      218 ValIleProSerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLys 237
Db      1444 GTTATATCCCATCTCTCTACTTCAATTAAGAGATTTATTAATCAACAGCTGTAA 1503
Qy      238 ThrIleIleTyrTyrAspSerGlnThrThrIleGluLysValSer-----CysGluMet 255
Db      1504 -----CTTCTTGCACTTACCAAGCACTTGCACAAAGATTAATTTTATGAGAAAT 1557
Qy      256 ArgTyrLysAlaThrThrAsnGlnThrTyrAsnValLysGluPheAspThrAsnPheThr 275
Db      1558 GAATTAAGAAATCT-----AATTCACTACAGAGCAGCGGAATGTCA 1602
Qy      276 Tyr-----ValGlnGlnSerGluPheTyr-----LeuGluProAsnIle 288
Db      1603 ATCAAGAGATTAAGAAATTAAGATTAATTTGCTGTGCAAGCAAGTATCCATACACT 1662
Qy      289 LysTyrValPheGlnValArgCysGlnGluThrGlyLysArgTyrTyrGlnProTyrSer 308
Db      1663 CTATATCTTTGAGATCGTGTGTTCTACTGAAACCTTCTGGAATGAGCAAAATGAGC 1722
Qy      309 SerProPheHisLysThrProGluThrValProGlnValThrSerLysAlaPheGln 328

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Db 1723 AATTAACCAACATTAAACAGAACCAAGCTCT-----TCAAAAGGG----- 1767
Qy 329 HtAspThrTrpAsnSerGlyLeuThrValAlaSerIleSerThrGlyHisLeuThrSer 348
Db 1768 CCGATCTCTGGAGA-----GAGTGAAGTTCT 1794
Qy 349 AspAsnArgGlyAspIleGlyLeuLeuGlyMetIleValPheAlaValMetLeuSer 368
Db 1795 GATCGAATA-----AATTATATATCTATGGAAGCCCTTTACCC 1833
Qy 369 IleLeuSerIleuIleGly-----IlePheAsnArgSerPheAsnThrGlyIleLeu 385
Db 1834 ATTATATAGAGCTATATGAAAAATATCTTCCATCATATATCTGTTCAATGATGAGGA 1893
Qy 386 ArgArgIleLeuLeuLeuIleProlysetrPleuTrgIu--AspIleProAsnMetIys 404
Db 1894 ACACAGTCCTTTCTGAAATCCCGATCCACAGCAAGAGAGATACCACTTGATTAAG 1953
Qy 405 AsnSerAsnValValIysMetLeuGlnGluAsnSer----- 416
Db 1954 AATGACTACATCATACAGCTAGTGGCTAAATTTCTGGGCTCATCACCACTTCCAA 2013
Qy 417 -----GluLeuMetAsnAsnAsn--SerSerGlnGlnValLeu----- 428
Db 2014 ATAGCGAGTATGGAATTCACAAATGATGATCTCAAAATAGAACAGTTGTGGAGATGGA 2073
Qy 429 -----TyrValAspProMetIleThrGlnIleGlyLeuIlePhe 441
Db 2074 AAGGGATTCCTCCTACCTGGCATTAAGACCCCAACATGACT----- 2115
Qy 442 IleProGlnHisIysProThrAspTyr-----LysIysGlnAsnThrGly 456
Db 2116 -----TGGACTACGCTCATTAAGTGGTGTAACTGCTCGGTCCGAA 2157
Qy 457 Pro-----LeuGlnThrArgAspTyrProGlnAsnSerIlePheAsnThrVal 474
Db 2158 CCATGCTTATGAGCTGAGAGAAAATTCTCTCAACAGCC-----ACTGAATCTGTA 2208
Qy 475 ValTyrIleProAspLeuAsnThrGlyTyrIysProGlnIleSerAsnPheLeuProGln 494
Db 2209 ATTAATCTGATGAGTTTCAGCCAGGTATAAGA-----TATAATTTTTCCTGTAT 2259
Qy 495 GlySerHisLeuSerAsnAsnGlnIleThrSerIle-----ThrLeu 509
Db 2260 GGAATGCAAAATCAAGATATCAATTAATGCTCCATGATGATATATAGAAATTTG 2319
Qy 510 LysProProValAspSerLeuAspSerGlyAsnAsnProArgLeuGlnIysHisProAsn 529
Db 2320 GCTCCCATTTGT-----GCAACCAAT 2340
Qy 530 PheAlaPheSerValSerSerValAsnSerLeu 540
Db 2341 TTTACTGTGAGATCTTCTGCAGATTCGATA 2373

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RESULT 15
US-10-511-937-3102
Sequence 3102, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Mohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946

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; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3102
; LENGTH: 5252
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3967)..(3988)
; OTHER INFORMATION: n t e a, c, g, t o r u
US-10-511-937-3102

Alignment Scores:
Pred. No.: 1.18e-07 Length: 5252
Score: 188.00 Matches: 109
Percent Similarity: 36.0% Conservative: 68
Best Local Similarity: 22.2% Mismatches: 184
Query Match: 5.7% Indels: 130
DB: Gaps: 26

US-10-667-289-2 (1-629) x US-10-511-937-3102 (1-5252)
Qy 111 GluThrIleuIleCysGlyLysAspIleSerSerGlyTyrProProAspIleProAspGlu 130
Db 1108 GAAGATACATATATTGGAACCGTTATTTTTCGATATCAACAGATCTCTCAACAA 1167
Qy 131 ValThrCysValIleTyrGlnTyrSerGlyAsnMetThrCysThrTrpAsnAla***Lys 150
Db 1168 GTCAATGTGAGACACATGATTTAAA--GAATATATATGTGATGAAATCCAGAGAG 1224
Qy 151 LeuThrTyrIle-----AspThrLysTyrVal----- 159
Db 1225 GTGACAGCGTTGGTGGGCCACGCTGCTACAACTTACCTTAAAGTTTTCAGGA 1284
Qy 160 -----ValHisValIysSerLeuGlnTyrGlnGlnGlnIleThrLeuThrSer 177
Db 1285 AATATGTTAGACTTAAAGAGCTGAAGCACCTACAAACAAAGCTAT----- 1332
Qy 178 TyrIleAsnIleSerThrAspSerLeuGlnGlyLysLysTyrLeuValTrpValGln 197
Db 1333 -----CAATTATTAATTCAATGCTTCCAAATCAACAAATATATTAATTACTTGAAT 1386
Qy 198 AlaAlaAsnAlaLeuGlyMetGlnGlnIleuSerLysGlnLeuGlnIleHisLeuAspAspIle 217
Db 1387 GCTCACATCCGCTGGGTGATGATCAACATCAATTTTA--GTAAATTAATCACTGAATA 1443
Qy 218 ValIleProSerAlaValIleSerArgAlaGluThrIleAsnAlaThrValProLys 237
Db 1444 GTTATCCCATCTACTCTTCAATCAAGTGAAGATTTTAATCAACAGCTGTTAAA 1503
Qy 238 ThrIleIleTyrTrpAspSerGlnThrIleGlnLysValSer-----CysGlnMet 255
Db 1504 -----CTTCTCTGCACTTATACAGCAACTTTCGAAGATTAATTTTATATGAAAT 1557
Qy 256 ArgTyrIleValAlaThrThrAsnGlnIleThrAsnValLysLeuIlePheAsnThr 275
Db 1558 GAAATTAAGAACT-----AATTCAATCAAGAGCAGCGAAATGTCACA 1602
Qy 276 Tyr-----ValGlnIleSerGlnIlePheTyr-----LeuGlnProAsnIle 288
Db 1603 ATCAAGAGATTAAGAAATTAAGTATCTTGTGCTGCAACAACTTAATCACTACT 1662
Qy 289 LysTyrValPheGlnValArgCysGlnGlnThrGlyLysArgTyrTrpGlnProTrpSer 308
Db 1663 CTATATCTTCTGCAATCTGTTCTACTGAACCTTTCGAAGTGAAGCAATGAGGC 1722
Qy 309 SerProPheHisIysThrProGlnThrValProGlnValThrSerLysAlaPheGln 328

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Db 1723 AATTAAAAACAATTATTAACAAGACCAGTCT-----TCMAAGGG----- 1767
QY 329 HisAspThrTPraSerSerGlyLeuThrValAlaSerIleSerThrGlyHisLeuThrSer 348
Db 1768 CCGATACCTTGAGA-----GAGTGAAGTTC 1794
QY 349 AspaSerArgGlyAspIleGlyLeuLeuGlyMetIleValPheAlaValMetLeuSer 368
Db 1795 GATGGAATA-----AATTAAATATCTATTGGAAGCTTTACCC 1833
QY 369 IleuSerIleuIleGly-----IlePheAsnArgSerPheArgThrGlyIleLeu 385
Db 1834 ATTATAGACCTAATGAAAAATCTTCTTCAATGATGATGCTTTCATCAGATGAGGA 1893
QY 386 ArgArgIleLeuLeuIleProIleThrLeuThrGlu---AspIleProAsnMetLeu 404
Db 1894 ACACAGTCCCTTTCTGAAATCCCTGATCCAGCAAAAGACAGATACGATTGATAG 1953
QY 405 AsnSerAsnValValIysMetLeuGlnGluAsnSer----- 416
Db 1954 AATGACTACATCATCAGCGTAGTGCTAAATTTCTGGGCTCATCACCACTTCCAA 2013
QY 417 -----GluLeuMetAsnAsnAsn---SerSerGlnIleValLeu----- 428
Db 2014 ATAGCAGATATGAAATTCCAATGATGATCTCAAAATAGAACAAAGTTGGGATGGA 2073
QY 429 -----TyrValAspProMetIleThrGlnIleIysGlnIlePhe 441
Db 2074 AAGGGGATTCCTCTCACCTGGCATTAAGACCCCAACATGACT----- 2115
QY 442 IleProGlnHisIysProThrAspTyr-----LysLysGluAsnThrGly 456
Db 2116 -----TGGACTACGTCATTAAGTGTGTAACGTCGTCGGCGGA 2157
QY 457 Pro-----LeuGlnThrArgAspTyr-ProGlnAsnSerLeuPheAspAsnThrVal 474
Db 2158 CCATGCCCTTATGACCTGAGAAAAGTCCCTCAACAGC-----ACTGAAACTGTA 2208
QY 475 ValTyrIleProAspLeuAsnThrGlyTyrIysProGlnIleSerAsnPheLeuProGlu 494
Db 2209 ATAGAAATCTGATGAGTTTCGACCAAGTATTAAGA-----TATTAATTTTCTCTGTAT 2259
QY 495 GlySerHisLeuSerAsnAsnAsnGlnIleThrSerLeu-----ThrLeu 509
Db 2260 GGATGCGAATAATCAAGATATCAATATATACCTCCATGATGATGATATAGAAATTG 2319
QY 510 LysProProValAspSerLeuAspSerGlyAsnAsnProArgLeuGlnLysHisProAsn 529
Db 2320 GCTCCCATTTGTT-----GCACCAAT 2340
QY 530 PheAlaPheSerValSerSerValAsnSerLeu 540
Db 2341 TTCTACTGTGAGATACTTCTGCAGATTGATTA 2373
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Job time : 425 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 14, 2006, 14:34:36 ; Search time 312 Seconds

(without alignments)
5658.305 Million cell updates/sec

Title: US-10-667-289-2

Perfect score: 3326

Sequence: 1 MNXVTIQMDVIALVILFSW.....TYFPQNTLSEHFNRIISLEK 629

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWEB.epool/US1067289/runat_13102006_111538_24459/epq_query.fasta_1
-DB=Issued Patents NA -QPM=faetap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs803p -USER=US1067289 @CGN 1.1.307 @runat_13102006_111538_24459
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /EMC_Celerra_SIDS3/prodata/2/ina/1 COMB.seq.*
2: /EMC_Celerra_SIDS3/prodata/2/ina/5 COMB.seq.*
3: /EMC_Celerra_SIDS3/prodata/2/ina/6A COMB.seq.*
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5: /EMC_Celerra_SIDS3/prodata/2/ina/7 COMB.seq.*
6: /EMC_Celerra_SIDS3/prodata/2/ina/H COMB.seq.*
7: /EMC_Celerra_SIDS3/prodata/2/ina/PCTUS COMB.seq.*
8: /EMC_Celerra_SIDS3/prodata/2/ina/PP COMB.seq.*
9: /EMC_Celerra_SIDS3/prodata/2/ina/RE COMB.seq.*
10: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3324	99.9	2859	US-09-853-180B-1	Sequence 1, Appl1
2	256.5	7.7	2995	US-09-700-820C-17	Sequence 17, Appl1
3	216	6.5	4040	US-08-685-118-1	Sequence 1, Appl1
4	216	6.5	4040	US-08-915-495-1	Sequence 1, Appl1
5	216	6.5	4040	US-08-914-520-1	Sequence 1, Appl1
6	216	6.5	4040	US-09-949-016-1887	Sequence 1887, Ap
7	216	6.5	4040	US-09-543-679A-2896	Sequence 2896, Ap
8	216	6.5	6019	US-09-543-679A-2897	Sequence 2897, Ap

9	211	6.3	2754	2	US-08-825-558-5	Sequence 5, Appl1
10	211	6.3	2754	3	US-09-312-611-5	Sequence 5, Appl1
11	209	6.3	3085	3	US-09-023-655-1131	Sequence 1131, Ap
12	209	6.3	3085	3	US-09-949-002-47	Sequence 47, Appl
13	208	6.3	3085	3	US-09-949-002-250	Sequence 250, App
14	207	6.2	1977	2	US-08-825-558-3	Sequence 3, Appl1
15	207	6.2	3085	3	US-09-312-611-3	Sequence 4, Appl1
16	207	6.2	3085	3	US-08-795-473B-4	Sequence 4, Appl1
17	207	6.2	3085	3	US-09-439-856-4	Sequence 25, Appl1
18	207	6.2	3477	3	US-09-313-942-25	Sequence 25, Appl
19	207	6.2	3477	3	US-10-282-162-25	Sequence 25, Appl
20	207	6.2	3507	3	US-09-313-942-23	Sequence 23, Appl
21	207	6.2	3507	3	US-10-282-162-23	Sequence 23, Appl
22	206	6.2	2369	2	US-07-797-556-1	Sequence 1, Appl1
23	206	6.2	2369	2	US-08-308-881-1	Sequence 1, Appl1
24	206	6.2	2369	2	US-09-058-263-1	Sequence 1, Appl1
25	206	6.2	2369	2	US-09-059-099-1	Sequence 1, Appl1
26	206	6.2	2369	3	US-09-058-264-1	Sequence 1, Appl1
27	206	6.2	2369	3	US-09-455-962-1	Sequence 1, Appl1
28	206	6.2	2369	7	PCT-US95-06530-1	Sequence 1, Appl1
29	190	5.7	2724	3	US-09-949-016-4257	Sequence 4257, Ap
30	188	5.7	3182	2	US-07-797-556-5	Sequence 5, Appl1
31	188	5.7	3182	2	US-07-943-843-1	Sequence 1, Appl1
32	188	5.7	3182	2	US-08-347-003-1	Sequence 1, Appl1
33	188	5.7	3591	2	US-07-943-843-5	Sequence 5, Appl1
34	188	5.7	5245	3	US-09-949-016-4210	Sequence 4210, Ap
35	188	5.7	5245	3	US-09-949-016-338	Sequence 338, App
36	188	5.7	5252	3	US-10-131-827-8827	Sequence 8827, Ap
37	188	5.7	5252	3	US-10-131-827-8827	Sequence 8827, Ap
38	188	5.7	5252	5	US-10-131-827-8827	Sequence 8827, Ap
39	188	5.7	5252	5	US-10-131-831-8828	Sequence 8828, Ap
40	188	5.7	5252	2	US-07-923-976-1	Sequence 1, Appl1
41	181.5	5.5	2498	2	US-07-943-843-3	Sequence 3, Appl1
42	171.5	5.2	2498	2	US-08-347-003-3	Sequence 3, Appl1
43	171.5	5.2	1724	3	US-09-071-224-5	Sequence 5, Appl1
44	170.5	5.1	1218	3	US-09-012-072-1	Sequence 1, Appl1
45	168.5	5.1				

ALIGNMENTS

RESULT 1
US-09-853-180B-1
Sequence 1, Application US/09853180B
Patent No. 6756481
GENERAL INFORMATION:
APPLICANT: Charitica, Madeline
APPLICANT: Parham, Christi L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OR INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
FILE REFERENCE: D01074
CURRENT APPLICATION NUMBER: US/09/853,180B
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 2859
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (119)..(2005)
FEATURE:
NAME/KEY: misc feature
LOCATION: (127)..(127)
OTHER INFORMATION: k means g or t/u.
OTHER INFORMATION: originally filed.
FEATURE:
NAME/KEY: mat peptide
LOCATION: (188)..(2005)

See page 12, line 34, of patent application at

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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (563)..(563)
; OTHER INFORMATION: r means g or a. See page 12, line 36, of patent application as
; OTHER INFORMATION: originally filed.
US-09-853-180B-1

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Alignment Scores:
Pred. No.: 0 Length: 2859
Score: 3324.00 Matches: 629
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 3 Gaps: 0

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US-10-667-289-2 (1-629) x US-09-853-180B-1 (1-2859)

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QY 21 CysHISGLYGLYIleThrAsnIleAsnCySerGlyHISileTrpValGluProAlaThr 40
Db 179 TGTCAATGAGAAATTACAAATATTAATCTGCTGGCCATCTGGTGAACCAAGCCACA 238
QY 41 IlePheLysMetGlyMetAsnIleSerIleTyrCysGlnAlaAlaIleLysAsnCySerGln 60
Db 239 ATTTTAAAGATGGGTATGAATATCTCTATATATTCGCAAGACAGCAATTAAGAATCGCAA 298
QY 61 ProArgLysLeuHISpHeTyrLysAsnGlyIleLysGluArgPheGlnIleThrArgIle 80
Db 299 CCAAGGAAACTCAATTTTATAAATAATGGATCAAGAAGATTTCAATCAACAAAGATT 358
QY 81 AsnLysThrThrAlaArgLeuTrpTyrLysAsnPheLeuGluProHISAlaSerMetTyr 100
Db 359 AATTAACCAACAGCTCGGCTTGGTATTAATAACCTTTCGAAACCACTGCTTCTATGTAC 418
QY 101 CysThrAlaGluCysProLysHISpHeGlnIleuThrLeuIleCysGlyLysAspIleSer 120
Db 419 TGCACCTGTAATGCCCAACATTTTCAAGAGACACTGATATGTGAAAAGACATTCT 478
QY 121 SerGlyTyrProProAspIleProAspGluValThrCysValIleTyrGluTyrSerGly 140
Db 479 TCTGGAATATCGCCAGATATCTCGATGAAGTAACTGTGCATTTTATGAATATTCAGGC 538
QY 141 AsnMetThrCysThrTrpAsnAla**LysLeuThrTyrIleAspTrpLysTyrValIle 160
Db 539 AACATGACTTGCACTGGAATGCTRGGAAGCTCACTACATAGACAAATATACGTGTA 598
QY 161 HisValLysSerLeuGluuThrGluGluGluGlnIleuThrLeuThrSerSerTyrIleAsn 180
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QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValIleProValGlnAlaAsn 200
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QY 201 AlaLeuGlyMetGluLysSerLysLeuGlnIleHisLeuAspAspIleValIlePro 220
Db 719 GCATTAAGCATGAGAGAGTCAAAACAACTGCATTAATCTCGATGATATAGTATACCT 778
QY 221 SerAlaAlaValIleSerArgAlaGluuThrIleAsnAlaThrValProLysThrIleIle 240
Db 779 TCTCAACCGCTCATTTCCAGGGCTGAGACTAATATGCTACAGGCCCAAGACCATATT 838
QY 241 TyrTrpAspSerGlnThrThrIleGluLysValSerCysGluMetCysArgTyrLysAlaThr 260
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QY 261 ThrAsnGlnThrTrpAsnValLysGluPheAspThrAsnPheThrTyrValGlnGluSer 280
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QY 301 LysArgTyrTrpGlnProTrpSerSerProPhePheHISLysThrProGluThrValPro 320
Db 1019 AAAAGGTACTGGAGGCTTGAGGTCCCGTTTTCATTAACCACTGAAACAGTTCCC 1078
QY 321 GlnValThrSerLysAlaPheGlnHISAspThrTrpAsnSerGlyLeuThrValIleSer 340
Db 1079 CAGGTACATCAAAAGATCTTCAACATGACACATGGAATTCGTGGCTTAACAGTTGCTCC 1138
QY 341 IleSerThrGlyHISLeuThrSerAspAsnArgGlyAspIleGlyLeuLeuGlyMet 360
Db 1139 ATCTCTACAGGACCTTACTTCTGCAACACAGAGAGACATTCGACTTTTATGGAAATG 1198
QY 361 IleValPheAlaValMetLeuSerIleLeuSerLeuIleGlyIlePheAsnArgSerPhe 380
Db 1199 ATGCTTGTGCTGTATGTGTCAATTCCTTTGATTTGGATATTTAACATCATCTTC 1258
QY 381 ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTrpLeuTyrGluAspIle 400
Db 1259 CGAAGCGGATTAAGAAGAGATCTTATGTATATCAAAAGTGGCTTATGAAGATATT 1318
QY 401 ProAsnMetLysAsnSerAsnValValLysMetLeuGlnLysAsnSerGluLeuMetAsn 420
Db 1319 CCTAATATGAAAAACAGCAATGTTGGAATAATCTACAGAAAAATAGTAACTTAAGAAAT 1378
QY 421 AsnAsnSerSerGluGlnValIleuTyrValAspProMetIleThrGluIleLysGluIle 440
Db 1379 AATTAATTCAGTGAAGAGTCTTATATGTTGATCCCATGATTCACAGATTAAGAAATC 1438
QY 441 PheIleProGluHISLysProThrAspTyrLysLysGluAsnThrGlyProLeuGluThr 460
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QY 501 AsnAsnGluIleThrSerLeuThrLeuLysProProValAspSerLeuAspSerGlyAsn 520
Db 1619 AATTAATGAATTAATCTTCACTTAACATTTAAACCAAGCTGATTCCTTAAGCTCAGGAAAT 1678
QY 521 AsnProArgLeuGlnLysHISProAsnPheAlaPheSerValSerSerValAsnSerLeu 540
Db 1679 AATCCCAAGTTTACAAAAGCATCTTAATTTGCTTTTCTGTTCAGATGTGAATTCATA 1738
QY 541 SerAsnThrIlePheLeuGlyLysLeuSerLeuIleLeuAsnGlnGlyCysSerSer 560
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QY 561 ProAspIleGlnAsnSerValGluGluGluuThrThrMetLeuLeuGluAsnAspSerPro 580
Db 1799 CCGACATACAAAACTCAGTAAAGAGAGAAACCAACCATGCTTTTGGAAAATGATTCACCC 1858
QY 581 SerGluThrIleProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIle 600
Db 1859 AGTGAACATATTCAGAAACAGACCCTGCTTCGATGAATTTTCTCTCTTTGGGGATC 1918
QY 601 ValAsnGluGluProSerIleAsnThrTyrPheProGlnAsnIleLeuGluSerHIS 620
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QY 621 PheAsnArgIleSerLeuLeuGluLys 629
Db 1979 TTCAATAGATTTCACTCTTGGAAAG 2005

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RESULT 2

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US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Teuchiya, Masaaki
; APPLICANT: Saito, Mikiyoshi
; APPLICANT: Ohtomo, Toshiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT APPLICATION NUMBER: US/09/700, 820C
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/JP99/02341
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(2839)
; US-09-700-820C-17

Alignment Scores:
Pred. No.: 1,1e-17 Length: 2995
Score: 256.50 Matches: 87
Percent Similarity: 43.3% Conservative: 65
Best Local Similarity: 24.8% Mismatches: 128
Query Match: 7.7% Indels: 71
DB: 3 Gaps: 17

US-10-667-289-2 (1-629) x US-09-700-820C-17 (1-2995)
QY 8 TTPAAspAlaValIleAlaLeuYrIleuPheserTrpCySHISglYglIleThrAsn 27
DB 107 TGCGTAGCCGAGACCTTGTCTTTTCTTCCACCACTAATCTATAGGCTCAACTT----- 160
QY 28 ILeAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheLysMetGlyMetAsn 47
DB 161 TTGGAAcCGTGTGTATCATCTACCCGAA---TTTCCAGTTGTCCACGCCGCGCTCAAC 217
QY 48 ILeSerIleTrpCys-----GlnAlaAlaIleLysAsnCyGlnProArgLysLeu 64
DB 218 TTCACGTCCATTTGTGTGTGAAGAGCGGTCTGTGCAG----- 256
QY 65 HIsPheTrpLysAsn-----GlyIleLysGluArg 74
DB 257 CATTTACTACCTGAATGACAGCTACATCGTGTGAAGAACCAACATGCTGTCTCCAGG 316
QY 75 PheGlnIleThrArgIleAsnLysThrAlaArgLeuTrpYrLysAsnPhelLeuGlu 94
DB 317 GAGCAAGCTCTGTCTATCAACAGACCACTCAGTCTACGTTCCACAGACGTGCTTC 376
QY 95 ProHIsAlaSerMetYrCyThrAlaGluCysProLysHisPheGlnIleuThrLeuIle 114
DB 377 CCGAGCGTGAGCTACACCTGCAACATCTGCTCTTGGCAGATCGAGCAAGAT---GTG 433
QY 115 CyGglYlyAspIleSerSerGlyYrProProAspIleProAspGluValThrCysVal 134
DB 434 TATGAGTCAACCACTTTCAGGCTTCTCCAGATTAACCTTCAAAATTTGACTTGCAAT 493
QY 135 IleTrpGluTrpSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrYrIle 154
DB 494 GTGAATAG---GGGAAGATATAGCTGTGCGAAGTGGAGACCCCGAAGAGAGACTTACCT 550
QY 155 AspThrLysTrpValValHisValLysSerLeuGluThrGluGluGlu----- 170
DB 551 GAAACAAACTACACT-----TTGAATACAGAGTGGCAACAGAGAGATTTCGTATGC 604

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QY 171 -----GlnIleTrpLeuThrSerSerYrIleAsnIle 181
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QY 182 SerThrAspSerLeuGlnIleGlyLysYrLeuValIleProValGlnAlaAlaAsnAla 201
DB 665 GAA-----GTCGGGTGGAGAGCAAGAAAGGCC 691
QY 202 LeuGlyMetGluGluSerLysGlnIleGlnIleHisLeuAspAspIleValIleProSer 221
DB 692 CTGGGAAGCTCTCCAGAGCTTATCAATTTTGACCCCGGTGATTAAGTAAAGCAACACC 751
QY 222 AlaAlaVal-----IleSerArgAlaGluThrIleAsnAlaThrValProLysThr 238
DB 752 CCACCATATATATTATTCAGTACGACCACTGAGGAATATTCAGTATATTAAG----- 805
QY 239 IleIleTrpTrpAspSerGlnThr-----IleGluLysValSerCySgluMetArg 256
DB 806 ---CTATCATGGGTCTCAGAGCGCTGGCGGCTTTAGATCTAAAGTGCATCAACAA 862
QY 257 TyrLeuAlaThrThrAsnGlnThrTP-----AsnValLysGluPhe 270
DB 863 TATAGACCAAGATGCTTCACCTTGATGATCCAGGTCCCTTGAAGATACAAATGCTCCT 922
QY 271 AspThrAsnPhetrpYrValGlnGlnSerGluPheTrpLeuGluProAsnIleLysYr 290
DB 923 CGAAGCTTCTTCACT---GTGAGAGAC-----CTCAAGCTTTTACAGAAATAT 967
QY 291 ValPheGlnValArg---CysGlnIleuThrGlyLysArgYrTrpGlnProLysSer 309
DB 968 GTGTTAGATGATCCGCTTCATTAAGACAGTGGAGAGGCTACGAGTCACTGAGTGAAG 1027
QY 310 ProPhePheHisLysThrProGluThrValPro 320
DB 1028 GAGGCTAGTGGAGCACTACAGAAAGACCA 1060

RESULT 3
US-08-685-118-1
; Sequence 1, Application US/08685118
; Patent No. 5840530
; GENERAL INFORMATION:
; APPLICANT: Gubler, Ulrich A
; APPLICANT: Presky, David H
; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,118
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Robert A.
; REGISTRATION NUMBER: 35,682
; REFERENCE/DOCKET NUMBER: CD 9195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-2863
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4040 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE: NO
 NAME/KEY: CDS
 LOCATION: 641..3226
 US-08-685-118-1

Alignment Scores:

pred. No.:	6.13e-13	Length:	4040
Score:	216.00	Matches:	75
Percent Similarity:	41.6%	Conservative:	57
Best Local Similarity:	23.7%	Mismatches:	131
Query Match:	6.5%	Indels:	54
DB:	2	Gaps:	13

US-10-667-289-2 (1-629) x US-08-685-118-1 (1-4040)

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Db 731 GGGGATGTACTGTGAAGCTTCCCATGTATTTACTTGATCCACTGCATATTTACA 790
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Qy 52 CyeGlnAlaAlaIleLysAsnCyGlnProArgLysLeuHisPheTyrlYsAsnGlyIle 71
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 791 TGC-----TCTTGAAAGCCGAGA-----808
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Qy 72 LysGlnArgPheGlnIleThrArgIleAsnLysThrAlaArgLeuTrpYrLys--- 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809 CAAGGCTGCTTACCTATTCACAGCTTACACAGTTA-----ATCCTGTACAAAGTTT 859
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 91 -----AsnPheLeuGlnProHisAla-----97
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 860 GACAGAAAGATCAATTTTACACATGGCCACTCCCTCAATTCTGAAGTACAGGCTTCCC 919
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 98 -----SerMetTyrlYrGthrAlaGlnCyProLysHisPheGlnGluThrLeu 113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 920 CTGGTACAACTGTGTTGTCTGCAAACTGGCCGT---ATCATATGTATGAAATTCAA 976
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 114 ILICyGlnLysAsnIleSerSerGlyTrpProArgLysIleProAsnGluValIthrCys 133
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Db 977 ATATGTGACAGACAGATCTTGCTGGTGGCTTCCCAACAGCTCAAAATTTATCTGTC 1036
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Qy 134 ValIleTyrlYrSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTrp 153
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Db 1037 ATACAGAAAGGAGAAACGGGAGCTGTGCTGCACCTGGGAAAGAGACAGACACCCAC 1096
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Qy 154 IleAspThrLysTrpValValHisVal-----LysSerLeuGlnThrGluGlu 170
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Db 1097 TTATACACTGATATCTTACAGCTAAGTACCAAAATTTAACTGGCAGAAAGCAA 1156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 171 GlnGlnTrpLeuThrSerSerTrp-----IleAsnIleSerThrAspSerLeu 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1157 TGTAAAGACATTTATGTGACTTATTTGACTTGGACTTGGAACTCACTGAAATTCCT 1216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 187 GlnGlyLysLysTrpLeuValTrpValGlnAlaIleAsnAlaLeuGlyMetGluGlu 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1217 GAA-----TCCATTTTACAGCAAGCTTACTGCTCAATGCTTGGAAAGTCTCT 1270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 207 SerLysGlnLeuGlnIleHisLeuAspAspIleValIleProSerAlaAlaValIleSer 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1271 TCATCTTCATTCACATTCACATTTCTTGACATAGTGAAGCTCTTCTCCGTGGACAT 1330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 227 ArgAlaGlnThrIleAsnAlaThrValProLysThrIleIleTyrlYrTPAspSerGlnThr 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1331 AGAATCAAAATTTCAAAGGCTTCGTGAGCAGATGATACCTTTATTCAGAGATGAGGA 1390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 247 ThrIleGlnLysValSerCysGlnMetArgTrpLysAlaThrThrAsnGlnThrTrpAsn 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1391 CTGGTA-----CTGCTTATTCAGCTCAGATATGGCCAGTAAACAGAGCTTGGAAAT 1444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 267 ValLysGlnPheAspThrAsnPheThrTrpVal-----GlnGlnSerGluPheTyrlLeu 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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Db 1445 ATG-----GTATATTTACAAAGGCCAAAGACATGATTTGCTGCATCTG 1492

Qy 285 GlnProAsnIleLysTrpValPheGlnValArgCysGln---GluThrGlyLysArgTrp 303

Db 1493 AAACATTTACAGAAATATGAATTTTCAGATTTCTCTCAAGTACATTTATTAAGGAAGT 1552

Qy 304 TrpGlnProTrpSerProPhePheHisLysTrpProGlnThrValPro 320

Db 1553 TCGAGTATGAGTGAATCATTCATTCAGAGCAACCAACGAGAAAGAGCTT 1603

RESULT 4

US-08-915-495-1
 Sequence 1, Application US/08915495

Patent No. 5852176
 GENERAL INFORMATION:

APPLICANT: Gubler, Ulrich A
 TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:

ADDRESSER: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street

CITY: Nutley
 STATE: NJ
 COUNTRY: USA

ZIP: 07110
 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,495

FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/685,118

FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Silverman, Robert A.
 REGISTRATION NUMBER: 35,682

REFERENCE/DOCKET NUMBER: CD 9195
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 235-2863
 TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 4040 base pairs
 TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO

ANTI-SENSE: NO
 FEATURE:

NAME/KEY: CDS
 LOCATION: 641..3226

US-08-915-495-1

Alignment Scores:

pred. No.:	6.13e-13	Length:	4040
Score:	216.00	Matches:	75
Percent Similarity:	41.6%	Conservative:	57
Best Local Similarity:	23.7%	Mismatches:	131
Query Match:	6.5%	Indels:	54
DB:	2	Gaps:	13

US-10-667-289-2 (1-629) x US-08-915-495-1 (1-4040)

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Qy 32 GLVHIEIETRPVAGIUPROALATNRIIEPHELYMEGLYMEASNIIESEIETRY 51
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 731 GGGGATGTACTGTGAAGCTTCCCATGTATTTACTTGATCCACTGCATATTTACA 790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
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Qy 52 CysGlnAlaAlaIleIysAsnCyGlnProArgLysLeuHisPheTyrLysAsnGlyIle 71
Db 791 TGC-----TCTTGAAGCCGAGA----- 808
Qy 72 LysGlnArgPheGlnIleThrArgIleAsnLysThrThrAlaArgLeuTyrLys--- 90
Db 809 CAAGGCGCTTTCACATTCCTCAGACGTACAAAGTTA-----ATCCGTACAAAGTTT 859
Qy 91 -----AsnPhleuGlnProHisAla----- 97
Db 860 GACAGAAAGATCAATTTTTCACATGCGCCTCTCAATTCCTCAAGTCACAGCTCTTCCC 919
Qy 98 -----SerMetTyrCyethrAlaGlnCyProLysHisPheGlnGluThrLeu 113
Db 920 CTGTGACAACTGTTGTCGTGAAACTGCGCTGT---ATCATATGATGAAATTCAA 976
Qy 114 IleCysGlyLysAspIleSerSerGlyTyrProProAspIleProAspGluValThrCys 133
Db 977 ATATGTGAGCAGAGATCTTGTGGTGGTGGCTCCAGAACAGCTCAAAATTTATCTGCG 1036
Qy 134 ValIleTyrGluTyrSerGlyAsnMetThrCyethrThrPheAsnAla***LysLeuThrTyr 153
Db 1037 ATACAGAAAGGAGAAACAGGGAGCTGCGCTGACCTGGGAAAGAGACGACAGACCCAC 1096
Qy 154 IleAspThrLysTyrValIleValIle-----LysSerLeuGlnThrGluGlu 170
Db 1097 TTATACCTGAGATCTTACCTTACAGCTTACGAGACCAAAATTTTACCTGCGACAGCAA 1156
Qy 171 GlnGlnTyrLysThrSerSerTyr-----IleAsnIleSerThrAspSerLeu 186
Db 1157 TGTAAAGACATTTATTTGATGATATTGGAATTTGGAATCAACCTCACCCCTGANTCACT 1216
Qy 187 GlnGlyLysLysLysTyrLeuValTTPValGlnAlaIleAsnAlaLeuGlyMetGluGlu 206
Db 1217 GAA-----TCCATTTTTCACAGCCAGGTTTACTCTCTCATATGCTTGAAGCTCTCT 1270
Qy 207 SerLysGlnLeuGlnIleHisLeuAspAspIleValIleProSerAlaAlaValIleSer 226
Db 1271 TCACCTTCATCCACATTCACATTCCTTGGACATATGAGGCTCTCTCCCTGGAGACATT 1330
Qy 227 ArgAlaGlnThrIleAsnAlaThrValProLysThrIleIleTyrTyrPaspSerGlnThr 246
Db 1331 AGAATCAAAATTTCAAAGGCTCCGTGAGCAGATGACCTTTATTTGAGAGATGAGGGA 1390
Qy 247 ThrIleGluLysValSerCyGlnMetArgTyrLysAlaThrThrAsnGlnThrTyrAsn 266
Db 1391 CTGGTA-----CTGCTTAATCGACTCAGATTTGCGCCAGTTAACAGCAGGCTCTGAAT 1444
Qy 267 ValLysGluPheAspThrAsnPheThrTyrVal-----GlnGlnSerGluPheTyrLeu 284
Db 1445 ATG-----GTTAATGTTTACAAAGGCCAAAGAGACATGATTGCTGAGATCTG 1492
Qy 285 GluProAsnIleLysTyrValPheGlnValArgCysGln--GluThrGlyLysArgTyr 303
Db 1493 AAACCATTTTACAGAAATATGATTTCAAGATTTCCCTTAAGTACATCTTTATTAAGGAAGT 1552
Qy 304 TTPGlnProTyrSerSerProPhePheHisLysThrProGluThrValPro 320
Db 1553 TGGAGTATGAGTGAATCATTTGAGAGACAAACACAGAAAGAGAGCCT 1603

```

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STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,520
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Robert A.
REGISTRATION NUMBER: 35,682
REFERENCE/DOCKET NUMBER: CD 9195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-2863
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4040 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 641..3226
US-08-914-520-1

Alignment Scores:
Pred. No.: 6.13e-13 Length: 4040
Score: 216.00 Matches: 75
Percent Similarity: 41.6% Conservative: 57
Best Local Similarity: 23.7% Mismatches: 131
Query Match: 6.5% Indels: 54
DB: Gaps: 13

US-10-667-289-2 (1-629) x US-08-914-520-1 (1-4040)
Qy 32 GlyHisIleTyrValGluProAlaThrIlePheLysMetGlyMetAsnIleSerIleTyr 51
Db 731 GCGAGTGTGACTGTGAAGCTTCCCATGTATTTTACTTGGATCCACTGTCATATTTACA 790
Qy 52 CysGlnAlaAlaIleIysAsnCyGlnProArgLysLeuHisPheTyrLysAsnGlyIle 71
Db 791 TGC-----TCTTGAAGCCGAGA----- 808
Qy 72 LysGlnArgPheGlnIleThrArgIleAsnLysThrThrAlaArgLeuTyrLys--- 90
Db 809 CAAGGCGCTTTCACATTCCTCAGACGTACAAAGTTA-----ATCCGTACAAAGTTT 859
Qy 91 -----AsnPhleuGlnProHisAla----- 97
Db 860 GACAGAAAGATCAATTTTTCACATGCGCCTCTCAATTCCTCAAGTCACAGGCTCTTCCC 919
Qy 98 -----SerMetTyrCyethrAlaGlnCyProLysHisPheGlnGluThrLeu 113
Db 920 CTGTGACAACTGTTGTCGTGAAACTGCGCTGT---ATCATATGATGAAATTCAA 976
Qy 114 IleCysGlyLysAspIleSerSerGlyTyrProProAspIleProAspGluValThrCys 133
Db 977 ATATGTGAGCAGAGATCTTGTGGTGGTGGCTCCAGAACAGCTCAAAATTTATCTGCG 1036
Qy 134 ValIleTyrGluTyrSerGlyAsnMetThrCyethrThrPheAsnAla***LysLeuThrTyr 153
Db 1037 ATACAGAAAGGAGAAACAGGGAGCTGCGCTGACCTGGGAAAGAGACGACAGACCCAC 1096

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Qy 518 -----SerGlyAsnAsnProArgLeuGlnLys 526
Db 2152 AAAATTAAGTGAAGACACAGCAGTGTATTGGGGGCTTCATCATGTATCTTCT 2211
Qy 527 HisProAsnPhenAlaPheSerValSerSerValAsnSerLeuSerThrIlePheLeu 546
Db 2212 AGGCCAAGATCTTCTACAGTGTATGAAAATGAATCTTCA---CAAAACCTCGAGCACT 2268
Qy 547 GlyGluSerLeuIleLeuAsnGlnGly---GluCysSerSerProApIleGln--- 564
Db 2269 GTCCAGATTCTTACCGGTGACACAGTGGCTACACAGACCAAGTCCGTCAAGTCAAGTC 2328
Qy 565 AsnSerValGluGluGlnThrThrMetLeuLeuGlnAsnAspSerProSerGluThrIle 584
Db 2329 TTCTCAAGATCCGAGCTACCCAGCCCTGTATTGAT-----TCAGAGAGACCGG 2376
Qy 585 ProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGlnGlu 604
Db 2377 CCAGAACATCTACAAATTAGTATGATCATGTATGAGCGGTATGATATTTGGCCAGGCAA 2436
Qy 605 LeuProSerIleAsnThrTyPheProGluAsnIleLeuGlu----- 618
Db 2437 -----CAGTACTTCAACAGAACTGCGACGTCAAGTCAATCAATCCAGAT 2481
Qy 619 ---SerHisPheAsnArg 623
Db 2482 ATTTCAATTTTGAAGG 2499

RESULT 10
US-09-312-611-5
; Sequence 5, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312.611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2754
; US-09-312-611-5

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Alignment Scores:
Pred. No.: 1,16e-12 Length: 2754
Score: 211.00 Matches: 172
Percent Similarity: 32.7% Conserved: 118
Beet Local Similarity: 19.4% Mismatches: 276
Query Match: 6.3% Indels: 320
DB: 3 Gaps: 44

US-10-667-289-2 (1-629) x US-09-312-611-5 (1-2754)
Qy 4 ValThrIleGlnThrPheAlaValIleAlaLeuTyIleLeuPheSerTrpCysHisGly 23
Db 4 TTACACCTTCGACGCTTGGGTAGTGAAGCAAGCTGTATTATTTCTCCACCACTGAATCTACA 63
Qy 24 GlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheLys 43
Db 64 GGTGAACCTCTAGATCCATGT---GGTTATATACGCTCGAA---TCTCAAGTTGTACAA 117
Qy 44 MetGlyMetAsnIleSerIleTyCysGlnAlaAlaIleLysAsnCysGlnProArgLys 63
Db 118 CTTCATTTCAATTTCACTGACGATTTGT-----GTCTAAAGGAAAAATGATGATGATTAT 171
Qy 64 LeuHisPheTyIleAsnGlyIle-----LysGlu 73
Db 172 TTTCATGTAAATGCTAAATTACATTTGCTGGAACCAACCATTTACTATTCCTTAAGAG 231
Qy 74 ArgPheGlnIleThrArgIleAsnLysThrAlaArgLeuTrpTyIleLysAsnPheLeu 93
Db 232 CAATATATCTATC-----ATTAACAGAACAGCATCCAGTGTCACTTACAGATATAGCT 285
Qy 94 GluProHisLeuSerMetTyCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113
Db 286 TCATTAATATTGAGCTCACTTGAACCATTTCTACATTCGACAGCTGAACAGTAAAGAT--- 342
Qy 114 IleCysGlyLysAspIleSerSerGlyTyProProAspIleProAspGluValThrCys 133
Db 343 GTTTATGATATCAACAATTAATTTGAGCTTCCCTCCAGAAAACCTAAATTTGAAGTTGG 402
Qy 134 ValIleTyGluTySerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTy 153
Db 403 ATGTGAACAG---GGAAAGAAATGAGGTGAGTGGATGGATGGAGGAAGAACACAC 459
Qy 154 IleAspThrLysTyValAlaHis----- 161
Db 460 TTGAGACAAACTTCACTTAAATCGAATGGCAACACAAAGTTGCTGATGCAAA 519
Qy 162 ---ValLysSerLeuGluThrGluGluGlnGlnIleuThrSerSerTyIleAsn 180
Db 520 GCAAAACGTGACACCCCACTCATGCACTGTGATTAATCTGATGTTTGTTCAC 579
Qy 181 IleSerThrAspSerLeuGlnGlyLysTyLeuValTrpValGlnAlaIleAsn 200
Db 580 ATTGA-----GTTGGGTGAAGCAGAGAAAT 606
Qy 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspAspIleVal----- 218
Db 607 GCCCTTGGGAAGTTACATCAGAT-----CATATCAATTTGATCTGTATTAAGTG 660
Qy 219 -----IleProSerAlaAlaValIleSerArgAlaGluThrIleAsnAlaThrVal 225
Db 661 AAGCCCAATCCGACATATTAATTAATCATGATCAATCAAGAGAAAGCTGTATATCTTA 720
Qy 236 ProLysThrIleIleTyTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253
Db 721 AAATTGACA-----TGGACCAACCCAGATTTAAGAGTGTATTAATCTAAATAAT 771
Qy 254 GluMetArgTyIleAlaThrThrAsnGlnThrTrpAsn---ValLysGluPheAspThr 272
Db 772 AACATTCATATAGAACCAAGATGCTCAACTTGGAGCCAGATTCCTCTGAAGACACA 831
Qy 273 AsnPheThrTyValGlnGlnSerGluPheTyLeuGluProAsnIleLysTyValPhe 292

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Db      832 GCATCCACCCGATCTTCATTCATGTCGCAAGACCTTAACCTTTTACAGAAATATGTGTT 891
Qy      293 GlnValArgCys---GlnGluThrGlyLeuArgPheProIleProIlePheSer----- 309
Db      892 AGGATTCGCTGATGATGAAGAGATGTAAAGGATACAGAGTACAGAGTGAAGAA 951
Qy      310 -----ProPhePheIleIlePhePro 316
Db      952 AGTGGATCACTTGAAGATAGACCATTAAGACCAAGTTCTGCTGATTAATAATGAT 1011
Qy      317 -----GluThrValPro----- 320
Db      1012 CCATCCCATCTCAAGGCTACAGAACTGTACAACCTCGTGGAGACATGGCCCTCTTTT 1071
Qy      321 GlnValThrSerIleValPheGlnIleAspThr-----TrpAsnSerGlyLeu 336
Db      1072 GAAGCCAAATGAAAATCTTGATTAATGATGACCTCTCACAGATGAAATCAATTA 1131
Qy      337 -----ThrVal---AlaSerIleSerThrGlyIleIleThrSerAspAsnArgGly 352
Db      1132 CAAATTTACACAGTTATGCGCAAAACCTGACAGTAATCTCACAATATGATCGC----- 1185
Qy      353 AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372
Db      1186 -----TATCTACCAACCTTAACAGTAAGAAATCTT 1215
Qy      373 IleGlyIlePheAsn----- 377
Db      1216 GTTGGCAATACAGATGAGCTGTTTAACTATCCCTGCTGATCTTCAAGCTACTCAC 1275
Qy      378 -----ArgSerPhe----- 380
Db      1276 CCTGTATGATCTTAAAGCATTCCTCCAAAGATTAACATGCTTGGGATGAGACTACT 1335
Qy      381 ---ArgThrGlyIleLeuArgArgIleLeuLeuLeuIleProIlePheLeuArgGly 399
Db      1336 CCAAGGGAATCTGTAAAGAAATATATCTT-----GAGTGTGT----- 1374
Qy      400 IleProAsnMetIleAsnSerAsnValValIleMetLeuGlnIleAsnSerGlyLeu 418
Db      1375 GTGTATTCAGATTAAGACCCCTGTATCAGACATGCGACAGAAAGATGATCCGTGCAT 1434
Qy      419 -----MetAsnAsnAsnSerSerGlyIleValIleLeuIleValIleAspPro 432
Db      1435 CGCACCATTTTAAGAGGAACTTAAGCAGAGCAAAATGCTATTGATTAACAGTTACTCCA 1494
Qy      433 MetIleThrGlu-----IleIleGlyIlePhe 441
Db      1495 GTATATGCTGATGAGACCAAGACCCCTGATCCATAAAGCATTCCTTAACAAGCT--- 1551
Qy      442 IleProGluIleIlePheProIleAspIleLeuIleValIleValIleValIleVal 458
Db      1552 CCACCTTCCAAAGACCTACTGTGCGCAAAAAAAGTAGGAAAAAAGCAAGCTGTCTTA 1611
Qy      459 GluThrArgAspIlePro-----GlnAsnSerIlePheAsnThrIleValIleVal 475
Db      1612 GAGTGGACCAACTCTCTGTTGATGTTCAAAATGATTTATCAGAAATTAATATATTTT 1671
Qy      476 Tyr----- 476
Db      1672 TATAGAACATCATTTGGAATAAAGTGTGTGAATGTGATTTCTTCCACAGAAATAT 1731
Qy      476 ----- 476
Db      1732 ACAATTGCTCTTGAAGTACACATTTGATGATGATGATGATGATGATGATGATGAT 1791
Qy      476 ----- 476
Db      1792 GAAGGTGGAGAGATGTCCAGAAATTCATTTTACTACCCCAAGTTTGTCTCAAGAGAA 1851
Qy      476 ----- 476
Db      1852 ATTGAAGCATATAGTCTGCTGTTGCTTGAAGTCTTCTATTCACAACTCTTGTGGAGTG 1911

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Qy      477 -----IleProAsp 479
Db      1912 CTGTTCTGCTTAAATAAGCAGACCTAATTAATAAACAATCTGCTAATGTCCAGAT 1971
Qy      480 LeuAsnThrGlyIleIlePheProIleIleSer-----AsnIleLeu 492
Db      1972 CTTCAAGAGATCATATATGCGCAGTGTCACTCACACTCTCCCAAGCACAATTTAAT 2031
Qy      493 ProGluIleSerIleIleAsnAsnAsn-----GluIleThr 505
Db      2032 TCAAAAGATCAAAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 2091
Qy      506 SerLeuThrLeuIlePro-----ProValAsp-----SerLeuAsp 517
Db      2092 GCAAATGACAAAAGCTTTTCCAGAAATCTGAATTAATGATGATGATGATGATGATGAT 2151
Qy      518 -----SerGlyAsnAsnProArgLeuGlnIle 526
Db      2152 AAATTAATACAGAGACACAGCAGTGTATGAGGAGGCTTCATCATGATCATCTTCT 2211
Qy      527 HisProAsnPheAlaPheSerValSerSerValAsnSerLeuSerAsnThrIlePheLeu 546
Db      2212 AGGCCAAGCATTTCTGACAGTGAATAATGATTTCA---CAAAACACTTGCAGACT 2268
Qy      547 GlyIleLeuSerLeuIleLeuAsnGlnGly---GlyCysSerSerProAspIleGln 564
Db      2269 GTCCAGATTTCTACCGGTGACACAGTGTACAGACACCAAGTCCCTGATCCAAATC 2328
Qy      565 AsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerProSerGluThrIle 584
Db      2329 TTCTCAAGATCGAGTCTACAGCCCTGTTGAT-----TCAGAGAGACGG 2376
Qy      585 ProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGluGlu 604
Db      2377 CCAGAAATCTACAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2436
Qy      605 LeuProSerIleAsnThrIlePheProGlnAsnIleLeuGlu----- 618
Db      2437 -----CAGTACTTCAACAGACACTGCAGTCAATGATCCAGATCCAGAT 2481
Qy      619 ---SerHisPheAsnArg 623
Db      2482 ATTTCACATTTGAAAGG 2499

RESULT 11
US-09-023-655-1131
; Sequence 1131, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/023,655
; CLASSIFICATION:
; PRIORITY DATA:

```

APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1131:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3085 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g186353
 US-09-023-655-1131

Alignment Scores:

Pred. No.:	2,35e-12	Length:	3085
Score:	209.00	Matches:	172
Percent Similarity:	32.7%	Conservative:	118
Best Local Similarity:	19.4%	Mismatches:	276
Query Match:	6.3%	Indels:	320
		Gaps:	44

US-10-667-289-2 (1-629) x US-09-023-655-1131 (1-3085)

QY 4 ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrpCysHisGly 23
 Db :::::|||||
 259 TTGACGTGGACGACTGGGTGTCAGACGCTGTTATTTCCACACGATGATTCACA 318
 QY 24 GlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheLys 43
 Db :::::|||||
 319 GGTAACTTCTAGATCCATGT---GGTTATATCATGCTCTGAA---TCTCCAGTGTACAA 372
 QY 44 MetGlyMetAsnIleSerIleTyrCysGlnAlaIleValIleValAsnGlyGlnProArgLys 63
 Db :::::|||||
 373 CTTATCTTAATTTTCACTGCACGTTGT-----GTCTAAAGAAAAATGATGATATAT 426
 QY 64 LeuHisPheTyrLysAsnGlyIle-----LysGlu 73
 Db :::::|||||
 427 TTTCATGTAATGCTAATTAATTCATTGTCGAAACAAACATTTTACTATTCCTAAAGAG 486
 QY 74 ArgPheGlnIleThrArgIleAsnLysThrAlaArgLeuTyrTyrLysAsnPheLeu 93
 Db :::::|||||
 487 CAATATATCTATC-----ATTAACGAAACAGCATCCAGTGTCACTTACGATATAGCT 540
 QY 94 GluProHisAlaSerMetTyrCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113
 Db :::::|||||
 541 TCATTAATATATTCAGCTCAGCTGCAACATTTTACATTCGACACGCTTGAACAGAAAT--- 597
 QY 114 IleCysGlyLysAspIleSerSerGlyTyrTrpProAspIleProAspGluValThrCys 133
 Db :::::|||||
 598 GTTATATGGAATCAACATATATTTCAAGCTGCTCCAGAAAAAAGCTTAAATTTGAGTTGC 657
 QY 134 ValIleTyrGluTyrSerGlyAsnMetThrCysThrTrpAsnAla***LysLeuThrTyr 153
 Db :::::|||||
 658 ATTGTGACGAG---GGGAAGAAATATGAGGTGATGAGTGTGGAAGGGAACACAC 714
 QY 154 IleAspThrLysTyrValIleHis-----Lys 161
 Db :::::|||||
 715 TTGAGAGCAAACTTCACTTAAATTCGATGAGGCAACACAAAGTTTGCATTCGAA 774
 QY 162 ---ValLysSerLeuGluThrGluGluGluGlnIleTyrLeuThrSerSerTyrIleAsn 180
 Db :::::|||||
 775 GCAAAAGGTGACACCCACCTGATGACGCTGATATATTTCTACCTGATGATTTGTCAAC 834
 QY 181 IleSerThrAspSerLeuGlnGlyLysLysTyrLeuValIleProValGlnAlaIleAsn 200
 Db :::::|||||

Db 835 ATGAA-----GTCTGGGTAGAACGACAGAT 861
 QY 201 AlaLeuGlyMetGluGluSerLysGlnLeuGlnIleHisLeuAspPheIleVal----- 218
 Db :::::|||||
 862 GCCCTTGGAAAGTTTACATCATGAT-----CATATCAATTTTGAATCCTGATATTAAGTG 915
 QY 219 -----IleProSerAlaIleValIleSerArgAlaGluThrIleAsnAlaThrVal 235
 Db :::::|||||
 916 AAGCCCAATCCGCACATATTTATATGATGATCACTGATCAAGACAGACATGCTAGATCTTA 975
 QY 236 ProLysThrIleIleTyrTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253
 Db :::::|||||
 976 AAATTGACA-----TGACCAACCAAGATTAAGAGTGTATTAATACATAAATAT 1026
 QY 254 GluMetArgTyrLysAlaThrThrAsnGlnThrTrpAsn---ValLysGluPheAspThr 272
 Db :::::|||||
 1027 AACATTCAATTAAGACCAAAAGATGCTCACTTGAAGCCAGATTCCTCTGAAGACACA 1086
 QY 273 AsnPheThrTyrValGlnGlnSerGluPheTyrLeuGluProAsnIleLysTyrValPhe 292
 Db :::::|||||
 1087 GCATCCACCCGATCTTCAATTCACGTGTCCAAGACCTTAAACCTTTTACAGAAATATGTGTT 1146
 QY 293 GlnValArgCys---GlnGluThrGlyLysArgTyrTrpGlnProTrpSerSer----- 309
 Db :::::|||||
 1147 AGGATTCGCTGTATGAAGAAAGATGTGAAGATACCTGAGTCACTGAGTGAAGAAAGCA 1206
 QY 310 -----ProPhePheIleLysThrPro 316
 Db :::::|||||
 1207 AGTGGATCACCTATGATAGATAGACCATTAAGACCAAGTTTCTGGTATTAATATGAT 1266
 QY 317 -----GluThrValPro----- 320
 Db :::::|||||
 1267 CCATCCCATCTCAAGCTACAGAACTGTACAACCTGTGTGGAAGACATTCCTCTTTT 1326
 QY 321 GlnValThrSerLysAlaPheGlnHisAspThr-----TrpAsnSerGlyLeu 336
 Db :::::|||||
 1327 GAAGCCAAATGGAATAATCTTGATTTGAAGTACTCTCAAGATGAAATACATTTA 1386
 QY 337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352
 Db :::::|||||
 1387 CAAAATTAACAGATTATGTCACAAACAGCATGAATATTCACAAATGATCC----- 1440
 QY 353 AspIleGlyLeuLeuGluGlyMetIleValIlePheAlaValMetLeuSerIleLeuSerLeu 372
 Db :::::|||||
 1441 -----TATCTAGCAACCTTACAGTAAAGAAATCTT 1470
 QY 373 IleGlyIlePheAsn----- 377
 Db :::::|||||
 1471 GTTGGCAAAATCAGATGCAAGCTGTTTAACTATCCCTGCTGTGACTTCAAGCTACAC 1530
 QY 378 -----ArgSerPhe----- 380
 Db :::::|||||
 1531 CCGTATATGATCTTAAAGCATTCGCCAAAGATTAACATGCTTTGGGTGGAATGAGACTACT 1590
 QY 381 ---ArgThrGlyIleLysArgArgIleLeuLeuLeuIleProLysTyrPheLysArgLys 399
 Db :::::|||||
 1591 CCAAGGGAATCTGTAAAGAAATATATACTT-----AGATGCTGT----- 1629
 QY 400 IleProAsnMetLysAsnSerIleValIleValMetLeuGlnGluAsnSerGluLeu--- 418
 Db :::::|||||
 1630 GTGTATACGATTAAGACACCTGATATACAGACTGCAACAGAAAGATGATCCGTGCAT 1689
 QY 419 -----MetAsnAsnAsnSerSerGluGlnValLeuTyr-----ValAspPro 432
 Db :::::|||||
 1690 CGCACCTATTAAGAGGAAGCTTACAGAGAGCAAGAAATGCTATTTGATTAACAGTTACTCCA 1749
 QY 433 MetIleThrGlu-----IleLysGluIlePhe 441
 Db :::::|||||
 1750 GTATATGCTATGAGACAGAGAACCTGATATCATTAAGCATACCTTAACAAGACT--- 1806
 QY 442 IleProGluHisLysProThrAspTyrLysLys-----GluAsnThrGlyProLeu 458
 Db :::::|||||
 1807 CCACCTTCCAAAGGACCTACTGTTCGACCAAAAAAGTAGGAAAAAGCAAGCTGTCTTTA 1866


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Db      916 AACCCACCGCCACATTAATTATCATCACTCAAGACCAAGCTGTATGCTTA 975
Qy      236 ProlyserThrlleIleTyrrPaepSerGlnThr-----ThrIleGluValSerCys 253
Db      976 AATATGACA-----TGACCAACCCAGTATTGAAGGTGTTATTAATCTTAATAT 1026
Qy      254 GluMetArgTyrrValalThrThrAsnGlnThrTripan--VallysgIuIleAspThr 272
Db      1027 AACATTCATATATAGACCAAGATGCTCAACTTGAGACAGATTCCTCTGAAGACACA 1086
Qy      273 AsnPhenThrTyrrValGlnGlnSerGluPhenTyrrleuGluProAsnIleTyrrValPhe 292
Db      1087 GCATCCACCCGATCTTCATTCACGTCCAAAGACCTTAACCTTTACAGATATGTTT 1146
Qy      293 GlnValArgCys--GlnGluThrGlyValArgTyrrGlnProTriPseSer----- 309
Db      1147 AGCATTCGCTGTATGAAGAGAGATGTATAGGATACCTGAGTACTGATGAAGAAAGCA 1206
Qy      310 -----ProPhePheIleTyrrThrPro 316
Db      1207 AGTGGATCATATGAAAGATAGACATTAAGACCAAGTTCTGTATTAATAATAGAT 1266
Qy      317 -----GluThrValPro----- 320
Db      1267 CCATCCCATCTCAAGGCTACAGAACTGTACAACTCGTGTGAGAGACATGCTCTTTT 1326
Qy      321 GlnValThrSerIlysalPheGlnIleAspThr-----TripanSerGlyLeu 336
Db      1327 GAAGCCATGGAATAATCTTGATATGAAAGTACTCACAAGATGGAATCATTTA 1386
Qy      337 -----ThrVal--AlaSerIleSerThrGlyIleuThrSerAspAsnArgGly 352
Db      1387 CAATATTACACAGTTATGCCACAAACTGACAGTAAATCTCAAAATGATCGC----- 1440
Qy      353 AspIleGlyLeuLeuGluMetIleValPheIleValIleMetLeuSerIleLeuSerLeu 372
Db      1441 -----TATCTGACCAACCTTACAGTAAGTAAGAAATCTT 1470
Qy      373 IleGlyIlePheAsn----- 377
Db      1471 GTTGGCAATACAGATGACGCTTTTAATATCCCTGCTGTACTTCAAGCTACAC 1530
Qy      378 -----ArgSerPhe----- 380
Db      1531 CCTGTATGATCTTAAGACATTCGCCAAAGATACATGCTTGTGGTGAATGACTACT 1590
Qy      381 ----ArgThrGlyIleValArgGlyIleLeuLeuIleProlyserTriPleuTyrrGluAsp 399
Db      1591 CCAAGGGAATCTGTAAAGAAATATATACTT-----GAGTGTGT----- 1629
Qy      400 IleProAsnMetIlysaSerAsnValIleValMetLeuGlnIleAsnSerGluLeu--- 418
Db      1630 GTGTATCAAGATTAAGACCCCTGTATCAGACACTGCGACACAAAGATGATCCGTGCAT 1689
Qy      419 -----MetAsnAsnSerSerGluGlnValLeuTyrr-----ValAspPro 432
Db      1690 CGCAGCTATTAAGAGGAACTTAGCAGAGCAAGATGCTATTTGATTAACGTTACTCA 1749
Qy      433 MetIleThrIle-----IleValGluIlePhe 441
Db      1750 GTATATGCTATGACGACGAGAGCCGTGAATCCATAAGGATACCTTAACAGACT--- 1806
Qy      442 IleProGluIleValysProThrAspTyrrIlyValys-----GluAsnThrGlyProLeu 458
Db      1807 CCACCTTCCAAAGACCTTACTGTTCCGACAAATAAGTGAAGAAAAAGAGAGCTGCTTA 1866
Qy      459 GluThrArgAspTyrrPro-----GlnAsnSerLeuPheAsnThrThrValVal 475
Db      1867 GAGTGGACCAACTTCTGTGTATGTTCAGAAATGATTTATCAAAATTAATATATATTT 1926
Qy      476 Tyr----- 476

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Db      1927 TATGAACATCATTTGGAAATGAATACTGCTGTGAATGTGATTTCTCCACAGAAATAT 1986
Qy      476 ----- 476
Db      1987 ACATTTGCTCTTGAAGTATGACATTTGATGATGATGAGATGACAGAT 2046
Qy      476 ----- 476
Db      2047 GAAGTGGAGAGATGTCCAGAAATTCATTTTACTACCCCAAGTTTGTCAAGAGAA 2106
Qy      476 ----- 476
Db      2107 ATTGAAGCATTAAGTGTGCTGTTGCTTATGCAATTCCTATGCAACTCTTCTGGAGTG 2166
Qy      477 -----IleProAsp 479
Db      2167 CTGTCTGCTTAATAAGGAGACCTAATTAATAAACATCTGCTGCTAATGTTCCGAT 2226
Qy      480 LeuAsnThrGlyTyrrIlyProGlnIleSer-----AsnPhenLeu 492
Db      2227 CCTTCAAGAGATATTTGCCAGTGTCTCCTCAGACTCTCCCAAGCAATTTTAAT 2286
Qy      493 ProGluGlySerIleSerAsnAsnAsn-----GluIleThr 505
Db      2287 TCMAAGATCAAAATGATTCAGATGCGCATTTTCACTGATCTAAGTGTGTGGAATAGAA 2346
Qy      506 SerLeuThrIleuIlyPro--ProValAsp-----SerLeuAsp----- 517
Db      2347 GCAATGACAAAAAGCCTTTTCCAGAAAGATCTGAATTCATTTGACCTGTTCAAAAAGAA 2406
Qy      518 -----SerGlyAsnAsnProAsnGluIly 526
Db      2407 AAATTAATATCTGAAGACACACAGCTGTATTTGGGGGCTTCATGATGATCTTCT 2466
Qy      527 HisProAsnPhenAlaPheSerValSerSerValSerSerIleThrIlePheLeu 546
Db      2467 AGGCGACAGCTTCTTACAGTATGAAATGAATCTTCA--CAAAACCTTGAGACACT 2523
Qy      547 GlyGluLeuSerLeuIleLeuGlnGly--GluCysSerSerProAspIleGln--- 554
Db      2524 GTCCAGATTTCTACCGGTGACACAGTGTGCTACAGACACCAAGTTCGTGACGCAAGTC 2583
Qy      565 AsnSerValGluGluGluThrThrMetLeuLeuGluAsnAspSerProSerGluThrIle 584
Db      2584 TTCTCAAGATCCAGTCTACCCAGCCCTGTGTAGAT-----TCAGAGAGCGG 2631
Qy      585 ProGluGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGluGlu 604
Db      2632 CCGAAGATCTTACAAATTAAGATCATGTATGATGCGGTGATGATTTTGGCCAGGCA 2691
Qy      605 LeuProSerIleAsnThrTyrrPheProGlnAsnIleLeuGlu----- 618
Db      2692 -----CAGTACTTCAACAGAACTGCGAGCATGAATCCAGTCCAGAT 2736
Qy      619 ---SerHisPheAsnArg 623
Db      2737 ATTTCACATTTGAAAGG 2754

RESULT 13
US-09-949-002-250
/ Sequence 250, Application US/09949002
/ Patent No. 690016
/ GENERAL INFORMATION:
/ APPLICANT: VENTUR, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
/ TITLE OF INVENTION: AND USES THEREOF
/ FILE REFERENCE: CL000790
/ CURRENT APPLICATION NUMBER: US/09/949,002
/ PRIOR APPLICATION NUMBER: 60/231,401
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 10823

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? SOFTWARE: Fastseq for Windows Version 4.
? SEQ ID NO 250
? LENGTH: 3085
? TYPE: DNA
? ORGANISM: Human
US-09-949-002-250

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Alignment Scores:

Pred. No.:	3,056-12	Length:	308
Score:	208.00	Matches:	178
Percent Similarity:	32.7%	Conservative:	118
Best Local Similarity:	19.4%	Mismatches:	276
Query Match:	6.3%	Indels:	320
DB:	3	Gaps:	44

US-10-667-289-2 (1-629) X US-09-949-002-250 (1-3085)

Qy	4	ValHxrllegIntPrApRAlValIleAlaLeuYrIleLeuPheSerTrpCysHleGly	23
Db	259	TTGACGTTGCAGACTGGCTAGTGCAGAACCCCTGTTATTTCTCAGACCACTGAATCTACA	318
Qy	24	GlyIleThrAenIleAenCysSerGlyHisIleTrpValGluProAlaThrIlePheLys	43
Db	319	GGTGAACCTTCAGATCCCATGT---GGTATATCAGTCCCTGA---TTCCTCAGTTGACAA	372
Qy	44	MetGlyMetAenIleSerIleTy-CysGlnAlaAlaIleLysAenCysGlnProArgLys	63
Db	373	CTTCAATCTCAATTTCCACTGCAAGTTGT-----GTGCTAAAGAAATAATGTATGATAT	426
Qy	64	LeuHisPheTyLysAenGlyIle-----LysGlu	73
Db	427	TTTCATGTAATATGCTAATTAACATTTCTCGAAAAACAACATTTACTATTCTTAAGAG	486
Qy	74	ArgPheGlnIleThrArgIleAenLysThrAlaArgLeuTrpTyLysAenPheLeu	93
Db	487	CAATATCTATC-----ATAAACGAAAGAGCATGCACTGTCACCTTTAACATATAGCT	540
Qy	94	GluProHisAlaSerMetTyCysThrAlaGluCysProLysHisPheGlnIleuThrLeu	113
Db	541	TCATTAATATATTCAGCTCACTTGCACAACCTTACATTCGGACAGCTTGACATGAT---	597
Qy	114	IleCysGlyLysAenIleSerSerGlyTyProProAenIleProAenGluValThrCys	133
Db	598	GTTATATGGAATCACATATATTTCAAGCTTGCTCCAGAAAAACCTAAATAATTGAGTGC	657
Qy	134	ValIleTyGluTySerGlyAenMetThrCysThrTrpAenAla**LysLeuThrTy	153
Db	658	ATTGTGAACGAG---GGGAGAAATAATGAGTGTGAGTGGATGTGTGAAGGGAACACAC	714
Qy	154	IleAspThrLysTyValValHis-----	161
Db	715	TTGGAGACAAATTCATCTTAAATCTGAATGGGCAACACACAGTTGCTGATTCGAA	774
Qy	162	---ValLysSerLeuGluThrGluGluGluGlnGlyTyLeuThrSerSerTyrIleAen	180
Db	775	GCAAAAGGTGACACCCCACTGATGACGTGTGATATTTCACTGATGATTTGTCTAC	834
Qy	181	IleSerThrAspSerLeuGlnGlyLysLysTyTyLeuValTrpValGlnAlaAen	200
Db	835	ATTGAA-----GTCGTGGTGGAGAACAGAT	861
Qy	201	AlaLeuGlyMetGluLysSerTyGlnLeuGlnIleHisLeuAenAspIleVal-----	218
Db	862	GCCTTTGGGAAGTTACATCAGAT-----CATATCAATTTTGAATCCGTATATTAAGTG	915
Qy	219	-----IleProSerAlaAlaValIleSerArgAlaGluThrIleAenAlaThrVal	235
Db	916	AAGCCCAATCGCCGACATTAATTTATCAGTGTATCAACTCAGAGGAACGTCTGTATCTTA	975
Qy	236	ProLysThrIleIleTyTrpAspSerLinhR-----ThrIleGluLysValSerCys	253
Db	976	AAATTGACA-----TGGACCAACCAAGATTAAGAGGTATATATATCAATAAATAT	1026

OY	254	GLuHeArgYrYLySaLaThThAsnGlnThrPan----	VallyGluPheAspThr	272
Db	1027	AACATTCATATAGGACCAAGAAGGCCCAACTTGGAGCCAGATTCCCTCGAAGACCA	1086	
OY	273	AsnPheThrTYrValGlnGlnSerGluPheTYrLeuGluProAsnIleLyTYrValPhe	292	
Db	1087	GCATCCACCCGATCTTCACTTCACTGTCGAAGACCTTAAACCTTTTACAGAATATATGTGTTT	1146	
OY	293	GlnValArgCys---GlnGluThrGlyLeuArgTYrTrpGlnProTrpSerSer----	309	
Db	1147	AGGATTCGCTGTATGAAGGAAGATGGTAAAGGATAGTCGAGTGCATGAGTGAAGACCA	1206	
OY	310	-----ProPhePheIleLyThrPro	316	
Db	1207	AGTGGGATCACCTTGAAGATAGACCATCTAAAGACCAAGTTCTGGTATTAATAATAGAT	1266	
OY	317	-----GluThrValPro-----	320	
Db	1267	CCATCCCACTACTCAAGGCTACAGAACTGACATCGTGGTGAAGACATGCGCTCTTTT	1322	
OY	321	GlnValThrSerLyPaIaPheGlnHieAspThr-----TrpAsnSerGlyLeu	336	
Db	1327	GAAGCCCAATGGAATAAATCTTGATATATCAAGTGACTCTCACAGATGGAATATCATTATTA	1386	
OY	337	-----ThrVal-----AlaSerIleSerThrGlyIleLeuThrSerAspAsnArgGly	352	
Db	1387	CAAAATTAACAAGTAATATGTCACAAACCTGACAGTAATATACAAAGATGCGC----	1444	
OY	353	AspIleGlyLeuLeuLeuGlyMetIleValPheAlaValMetLeuSerIleLeuSerLeu	372	
Db	1441	-----TATCTAGCAACCTTAACAGTAAGAATCTT	1476	
OY	373	IleGlyIlePheAsn-----	377	
Db	1471	GTGGCAAAATCAGATGAGCTGTTTAACTATCCCTGCTGTGACTTCAAGCTACTAC	1530	
OY	378	-----ArgSerPhe-----	380	
Db	1531	CCTGTAAATGATCTTAAAGCAATTCGCCAAGATACATGCTTGGGTGAATGAGCTACT	1590	
OY	381	---ArgThrGlyIleLyArgArgIleLeuLeuLeuIleProLySTrpLeuTYrGluAsp	399	
Db	1591	CCAAAGGAATCTGTAAAGAAATATATACTT-----GAGTGGTGT-----	1622	
OY	400	IleProAsnMetLyAsnSerAsnValValLyMetLeuGlnGluAsnSerGluLeu----	418	
Db	1630	GTGTATTCAGATTAAGAACCCTGTATACAGACTGCGAACAAAGAAAGATGTAACCGTCA	1688	
OY	419	-----MetAsnAsnAsnSerSerGluGlnValLeuTYr-----ValAspPro	432	
Db	1690	CGCACCTATTATTAAGAGGAACCTTAGCAGAGAGCAAAATGCTATTGTATACAGTTACTCA	1749	
OY	433	MetIleThrGlu-----IleLyGluIlePhe	441	
Db	1750	GTAATATGCTGTAGGACCAAGAACCCGTGAATCCATAAGCATACCTTAAACAAGCT---	1806	
OY	442	IleProGluIleLyProThrAspTYrLyLyLyLy-----GluAsnThrGlyProLeu	458	
Db	1807	CCACTTCGCAAGAACCTCACTGTTGGACAAABAAGAGGAGAAAAGCAGCTGTCTTA	1866	
OY	459	GluThrArgAspTYrPro-----GlnAsnSerLeuPheAsnThrThValVal	475	
Db	1867	GAGTGGGACCAACTTCCTGTGATGATTCAGATGATTTATCAGAAAATTATATCATATATTT	1926	
OY	476	TYr-----	476	
Db	1927	TATAGAAACCATCATTTGAATAATGAATCTGCTGTGAATGTGATTTCTTCCACACAGAAATAT	1986	
OY	476	-----	476	
Db	1987	ACATTGTCTCTTTGACTAGTACACATGTGATACATGATGAAGATGAGACATACACAGAT	2046	
OY	476	-----	476	

Db 2047 GAAGTGGAGAGATGTCAGCAATTCATTCTTACTACCCCAAGTTGCTCAAGAGAA 2106
 476 ----- 476
 Db 2107 ATTGAAGCATTAGTCGTCCTGTTGCTTACATTCCTATTGACAACTCTTCTGGAGTG 2166
 477 ----- 479
 Db 2167 CTGTTCTGTTTATAAGCAGACCTATTAAAAACATCTGGCTTAATGTTCCAGAT 2226
 480 LeuAsnThrGlyTyrLysProGlnIleSer-----AsnPheLeu 492
 2227 CCTTCAAGAGATCATATGCGCAGTGTCTCACACTCTCCCAAGCACAATTTTAAT 2286
 493 ProGlnGlySerHisLeuSerAsnAsn-----GluIleThr 505
 2287 TCAGAAAGATCAAAATGATTAATGAGCAATTTCACTGATGTAAGTTGTTGGAAATAGAA 2346
 506 SerLeuThrLeuLysPro-----ProValAsp-----SerLeuAsp----- 517
 2347 GCAATGACAAAAAGCTTTTCCAGAAAGATCTGAATCATTTGACCTGTTCAAAAAAGAA 2406
 518 ----- SerGlyAsnAsnProAlaGluLeuLys 526
 2407 AAATTAATATCTAGAGACACAGCAGTGTATTGGGGGCTTCATGTCATGTCATCTTCT 2466
 527 HisProAsnPheAlaPheSerValSerSerValAsnSerLeuSerAsnThrIlePheLeu 546
 2467 AGGCAGACATTTCTAGCAGTGTAGTAAATGAATCTTCA-----CAAAACCTTTGAGACACT 2523
 547 GlyGluLeuSerLeuIleLeuAsnGlnGly-----GluCysSerSerProAlaIleGln--- 564
 2524 GTCCAGATTTCTACCGGTGATACACAGTGGCTTACAGACCAAGTCCGTGATGCCAAGTC 2583
 565 AsnSerValGluGlnGluThrThrMetLeuLeuGluAsnAspSerProSerGluThrIle 584
 2584 TTCTCAGATCCAGTCTACCCAGCCCTGTTAGAT-----TCAGAGAGCGG 2631
 585 ProGlnGlnThrLeuLeuProAspGluPheValSerCysLeuGlyIleValAsnGlnGlu 604
 2632 CCAAGACATCTACATTTAGTATGATCATGTGATGCGGTGATTTTCCAGGCA 2691
 605 LeuProSerIleAsnThrTyrPheProGlnAsnIleLeuGlu----- 618
 2692 -----CAGTACTTCAACAGACACTGACGATGATGATCAATCCAGTCAGAT 2736
 619 ---SerHisPheAsnArg 623
 2737 ATTTCACATTTTGAAAG 2754
 Db 2737 ATTTCACATTTTGAAAG 2754
 RESULT 14
 US-08-825-558-3
 Sequence 3, Application US/08825558
 Patent No. 5965724
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/825,558
 / FILING DATE: 19-MAR-1997
 / CLASSIFICATION: 536
 / ATTORNEY/AGENT INFORMATION:
 / NAME: ESMOND, ROBERT W.
 / REGISTRATION NUMBER: 32,893
 / REFERENCE/DOCKET NUMBER: 0623,0530001
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202)371-2600
 / TELEFAX: (202)371-2540
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1977 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: both
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 1..1974
 / US-08-825-558-3
 Alignment Scores:
 Pred. No.: 1,86e-12 Length: 1977
 Score: 207.00 Matches: 124
 Percent Similarity: 36.8% Conservative: 97
 Best Local Similarity: 20.6% Mismatches: 208
 Query Match: 6.2% Indels: 172
 DB: 2 Gaps: 32
 US-10-667-289-2 (1-629) x US-08-825-558-3 (1-1977)
 QY 4 ValThrIleGlnTrpAspAlaValIleAlaLeuTyrIleLeuPheSerTrpCysHisGly 23
 Db 4 TTACGTTGACAGCTTGGGTGATGTCAGAGCTTTGTTATTTCTCTCCACCACTGAATCTACA 63
 QY 24 GlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheLys 43
 Db 64 GGTGAATCTTACATCATGAT---GGTATATCAGTCTGAA---TCTCAGATTGACAA 117
 QY 44 MetGlyMetAsnIleSerIleTyrCysGlnAlaIleLeuAsnGlnProAlaGlyLys 63
 Db 118 CTTCATCTTAATTTCACTGCAAGTTGT-----GTCTAAAGGAAAAATGATGATTAAT 171
 QY 64 LeuHisPheTyrLysAsnGlyIle-----LysGlu 73
 Db 172 TTTCATGTAATGCTAATTTACATTTGCTGAAAAACAACATTTTACTATCTCTTAAGAG 231
 QY 74 ArgPheGlnIleThrArgIleAsnLysThrThrAlaArgLeuTrpTyrLysAsnPheLeu 93
 Db 232 CAATATATCATC-----ATTAACAGAACAGATCCAGTGTACCTTTACAGATATAGCT 285
 QY 94 GluProHisAlaSerMetTyrCysThrAlaGluCysProLysHisPheGlnGluThrLeu 113
 Db 286 TCATTAAATATTGAGTCACTTGCACATTTCTTACATTCGAGACAGCTTGAAACGAAT--- 342
 QY 114 IleCysGlyLysAsnIleSerSerGlyTyrProProAspIleProAspGluValThrCys 133
 Db 343 GTTTATGAAATTCACATTAATTTCAAGCTTCCCTCCGAAAAAATTTGAATGCTG 402
 QY 134 ValIleTyrGluTyrSerGlyAsnMetThrCysThrTrpAsnAla**LysLeuThrTyr 153
 Db 403 ATGTGAACAG---GGAAAGAAATGAGGTGTGAGTGGATGTGGAGAGGAAACACAC 459
 QY 154 IleAspThrLysTyrValValHis----- 161
 Db 460 TTGAGACAAACTTCACTTAAATCTGAATGGCAACACAAAGTTGCTGATTGCCAA 519
 QY 162 ---ValLysSerLeuGluThrGluGlnGlnIleTyrIleThrSerSerTyrIleAsn 180
 Db 520 GCAAAAGTGACACCCCACTGATGACCTGTTGATTTACTGTGATTTTGTGCAC 579


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Qy 181 IleserThraSerLeuGlnGlyLysLeuValTrpValGlnAlaAlaAsn 200
Db 580 ATTGAA-----GTCTGGTGAAGACGAGAT 606
Qy 201 AlaLeuGlyMetGluSerLysGlnLeuGlnIleHisLeuAspAlaVal----- 218
Db 607 GCCCTGGGAAGGTATACATGAT-----CATATCAATTTTGTGCTGATATATTAAGTG 660
Qy 219 -----IleProSerAlaAlaValIleSerArgLysGluThrIleAsnAlaThrVal 235
Db 661 AAGCCCAATCCCGCAATTAATTAATCACTGATCACTGAGCAATGCTGATGATCTTA 720
Qy 236 ProLeuThrIleLeuLysTrpAspSerGlnThr-----ThrIleGluLysValSerCys 253
Db 721 AATTTGACA-----TGACCAACCAAGTATTAAGAGTGTATTAATTAATTAAT 771
Qy 254 GluMetArgTrpLysAlaThrThrAsnGlnThrTrpAsn-----ValLysGluPheAspThr 272
Db 772 AACATCAATATAGACCAAAAGATGCTCAACCTTGAGACGAGATTCCTCTGAAGACACA 831
Qy 273 AsnPheThrTrpValGlnGlnSerGluPheTrpLeuGluProAlaIleLysTrpValPhe 292
Db 832 GCATCCACCCGATCTTCATTCATTCGTCMAAGACCTTAACCTTTTACAGAAATATGTTT 891
Qy 293 GlnValArgCys---GlnGluThrGlyLysArgTrpTrpGlnProTrpSerSer----- 309
Db 892 AGGATTCGCTGTATGAAGAGAGATGTATAGGATATCTGAGATCACTGAGTGAAGAAGCA 951
Qy 310 -----ProPhePheHisLysTrpThrPro 316
Db 952 AGTGGATCACTATGAAGATAGACATTAAGACCAAGTTTCTGTTTAAATAGAT 1011
Qy 317 -----GluThrValPro----- 320
Db 1012 CCATCCCATCTAGAGGCTACAGAACTGTACAACTGCTGTGAGAGACATTCCTCTTTT 1071
Qy 321 GlnValThrSerLysAlaPheGlnHisAspThr-----TrpAsnSerGlyLeu 336
Db 1072 GAAGCCATAGAAAATCTTGATTAAGAGTATGACCTCACAAGATGGAATCACTTTA 1131
Qy 337 -----ThrVal---AlaSerIleSerThrGlyHisLeuThrSerAspAsnArgGly 352
Db 1132 CAATATTACACAGTTATGTCACAAAACGACAGTAAATATCTCACAAATATGATCGC----- 1185
Qy 353 AspIleGlyLeuLeuGlnMetIleValPheAlaValMetLeuSerIleLeuSerLeu 372
Db 1186 -----TATCTACCAACCTTAACAGTAAAGAAATCTT 1215
Qy 373 IleGlyLysPheAsn----- 377
Db 1216 GTTGGCAATATCAGATGCACTGTTTAATATCTGCTGCTGATCTTCAAGCTACTCAC 1275
Qy 378 -----ArgSerPhe----- 380
Db 1276 CCGTATATGATCTTAAGCATTCCTCCAAAGATTAACATGCTTTGGGTGAATGAGCTACT 1335
Qy 381 ---ArgThrGlyLysValArgGlyLeuLeuLeuIleProLysTrpLysTrpGluAsp 399
Db 1336 CCAAGGGAATCTGTAAAGAAATATATATCTT-----GAGTGTGT----- 1374
Qy 400 IleProAsnMetLysAsnSerAsnValValLysMetLeuGlnGluAsnSerGluLeu--- 418
Db 1375 GTGTATCATAGATTAAGACCCCTGTATACAGACTGGCAACAGAAAGTGTACCGTGCAT 1434
Qy 419 -----MetAsnAsnAsnSerSerGluGlnValLeuTrp-----ValAspPro 432
Db 1435 CGCACTATTTAAGAGGAACTTACAGAGACAAATGCTATTTGATTAACAGTTACTCA 1494
Qy 433 MetIleThrLys-----IleLysGluIlePhe 441
Db 1495 GTATATGCTATGACCAAGAGCCCTGAATTCATTAAGCATATCACTTAACAGCT--- 1551
Qy 442 IleProGluHisLysProThrAspTrpLysLys-----GluAsnThrGlyProLeu 458

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Db 1552 CCACCTTCCAAAGACCTACTGTTCCGACAAAAAGTAGGAAAAAGAGCTGCTTA 1611
Qy 459 GluThrArgAspTrpPro-----GlnAsnSerLeuPheAsnThrThrValVal 475
Db 1612 GAGTGGGACCAACTCTCTGTTGATGTTTCAGAAATGATTATACAGAAATATATTAATTT 1671
Qy 476 Tyr 476
Db 1672 TAT 1674

RESULT 15
US-09-312-611-3
; Sequence 3, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: GP130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1974
; US-09-312-611-3

Alignment Scores:
Pred. No.: 1.86e-12 Length: 1977
Score: 207.00 Matches: 124
Percent Similarity: 36.8% Conservative: 97
Best Local Similarity: 20.6% Mismatches: 208
Query Match: 6.2% Indels: 172
Gaps: 32

US-10-667-289-2 (1-629) x US-09-312-611-3 (1-1977)
Qy 4 ValThrIleGlnThrAspAlaValIleAlaLeuTrpIleLeuPheSerTrpCysHisGly 23
Db 4 ThrACGTTCGACAGCTTGGGAGTGCAGAGCTTGTATTTCTCTACCACTGAATGTACA 63
Qy 24 GlyIleThrAsnIleAsnCysSerGlyHisIleTrpValGluProAlaThrIlePheLys 43
Db 64 GGTGAACCTTCTGATCCATGCT---GGTTATATCATGCTCGAA---TCTCCAGTTGTACA 117

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